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GenCore version 5.1.6
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- protein search, using sw model OM protein January 10, 2005, 21:05:23; Search time 153 Seconds (without alignments) 940.199 Million cell updates/sec Run on:

1 SNHGPDATEAEEDFVDPWTV.......VTDEIVKEFMTPRKLSFDFQ 401 US-09-813-718-10\_COPY\_71\_471 2116 score: Sequence: Title: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 segs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:\* geneseqp2001s:\* geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* A\_Geneseq\_23Sep04:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2004s:\* •• Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		non	TrpRS T1	Human sup	Human sup	His6-tagg	Human sup	Human min	Human min	His6-tagg	Human min	Novel hum	Human try	Cancer/an	Marker ge	Protein e	Human ful	Human try	Full leng	Human ful	Human pro	Human hea	Human pro	Pancreas	Lung canc	Human HCM	TrpRS T2
		nescription	Aag79549	Aab47617	Aae13493	Aag79548	Abu 72386	Aab47616	Aae13492	Aag79547	Abu72385	Adf76576	Abu64298	Adn39916	Adj75318	Adp12573	Aab47615	Aae13491	Aag79546	Abu72384	Ade25762	Adj69429	Ade76998	Adq30575	Aab58220	Aay05372	Aaq79541
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dР	Query	March	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.3	99.3	99.3	99.3	99.3	99.1	94.0
	3	arose	2116	2116	2116	2116	2116	2116	2116	2116	2116	2116	2116	2116	2116	2116	2116	2116	2116	2116	2101	2101	2101	2101	2101	2096	1988
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Aab47618 Human ina	Aael3494 Human ina	Aag79544 His6-tagg	Abu72387 Human min	_	Aag79953 T2-TrpRS.	_	Adj76140 Marker ge	_	Abb64621 Drosophil	Abb67203 Drosophil	Aag23698 Arabidops		•	Abp73795 Candida a	Abr53898 Protein a	Adk64828 Disease t	Abj26487 Aspergill		Aag23699 Arabidops
AAB47618	AAE13494	AAG79544	ABU72387	ADJ87004	AAG79953	ADB79825	ADJ76140	ADP04555	ABB64621	ABB67203	AAG23698	AAG23697	AAB66931	ABP73795	ABR53898	ADK64828	ABJ26487	ADB70160	AAG23699
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392	392	392	392	392	378	475	481	447	430	430	402	426	424	424	432	432	433	456	292
94.0	94.0	94.0	94.0	94.0	93.2	91.6	91.6	69.0	64.8	64.8	61.6	61.6	57.6	56.7	55.0	55.0	53.2	52.3	45.7
1988	1988	1988	1988	1988	1973	1938	1938	1459.5	1370.5	1370.5	1304	1304	1218.5	1200.5	1163	1163	1125	1107.5	968
56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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neovacular equipment diabetes; rubeotic glaucoma; retinopathy; ocular complication; diabetes; rubeotic glaucoma; retinopathy; prematurity; keratitis; ischaemic retinopathy; pathological myopic; ocular histoplasmosis; pterygia; T1; punitate innerchoroidopathy; retinal degeneration; growth factor; vascularisation; vascular endothelial cell function; angiogenesis.
                                                                      tryptophanyl-tRNA synthase; TrpRS; ocular neovascularisation;
AAG79549 standard; protein; 401 AA
                                    (first entry)
                                                      TrpRS Il polypeptide.
                                    10-DEC-2002
                  AAG79549;
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22-FEB-2002; 2002WO-US005185. WO200267970-A1. Homo sapiens. 06-SEP-2002.

(SCRI ) SCRIPPS RES INST.

23-FEB-2001; 2001US-0270951P.

Friedlander Schimmel P, Wakasugi K,

Ξ

WPI; 2002-698635/75.

New polypeptides derived from human tryptophanyl-tRNA synthase, useful for inhibiting ocular neovascularization in a patient, or for treating neovascular eye diseases, e.g. rubeotic glaucoma, retinopathy, keratitis, or pterygia.

Example 1; Page 78-79; 83pp; English.

This sequence represents a novel cleavage product, T1, of recombinant human tryptophanyl-tRNA synthase (TrpRS). A related cleavage product, T2, is water soluble and comprises residues 94-471 of full length TrpRS. The water-soluble T2 polypeptide is useful for inhibiting ocular neovascularisation in a patient. The T2 polypeptide is useful for treating neovascular eye diseases, e. T2 polypeptide is useful for treating neovascular eye diseases, representation, ocular complications of diabetes, rubeotic glaucoma, retinopathy of

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Schimmel P,

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                                                                                                                                                                                                                                                                                         LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 180
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                                                                                                                                                                                                                                                                                                                                                                                                 Tyrosyl-tRNA synthetase, TyrRS; Rossmann fold nucleotide binding domain; vascular endothelial cell function; burn; plastic surgery; abdomen; polymorphonuclear leucocyte elastase; angiogenesis; tumour metastasis; angiogenesis; graft; myocardial infarction; solid tumour; wound healing; dermal ulcer; diabetic ulcer; endothelialization;
 prematurity, keratitis, ischaemic retinopathy (e.g. sickle cell), pathological myopic, ocular histoplasmosis, pterygia, or punitate innerchoroidopathy. This polypeptide is particularly useful for treating retinal degeneration to prevent the damaging effects of trophic and growth factors, and for promoting vacularisation to retard retinal degeneration by enhancing blood flow to cells. These are also useful for regulating vascular endothelial cell function, and in particular, for
                                                                                                                                                                                                                           VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
                                                                                                                                                                                                            1 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH
(e.g. sickle cell),
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                                                                                                                                                     Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dermal ulcer; diabetic ulcer; endothelialization;
tryptophanyl-tRNA synthetase; trpRS; vascular graft surgery
                                                                                                                                                                                   Indels
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                                                                                                                                                       100.0%; Score 2116; DB 5;
100.0%; Pred. No. 1.6e-209;
ive 0; Mismatches 0;
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                                                                                                                                                                                      Matches 401; Conservative
                                                                                                      inhibiting angiogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human supermini TrpRS.
                                                                                                                                                                        Similarity
                                                                                                                             Sequence 401 AA;
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The sequences given in AAB47615-18 show full length and truncated versions of trptophanyl-tENNA synthetase (TrpRS). The truncated TrpRS of the invention comprises a Rosemann fold nuclecide binding domain, and is capable of regulating vascular endothelial cell function. It is of approx. 40 kilo balton molecular weight and is produced by cleavage of full length TrpRS with polymorphonuclear leucocyte elastase. Truncated till length TrpRS with polymorphonuclear leucocyte elastase. Truncated till length TrpRS with polymorphonuclear leucocyte elastase. Truncated argiogenesis to a graft, treating myocardial infarction, solid tumor, and angiogenesis to a graft, treating myocardial infarction, solid tumor, and andidopenesis to a graft, treating wounds such as dermal ulcers, diabetic condition that would benefit from increased angiogenesis a wound healing agent for treating wounds such as dermal ulcers, diabetic curcers, burns and injuries and in plastic surgery when reconstruction is cuscular in the treatment of abdominal wounds where there is high risk of unfection. Truncated TrpRS promotes endothelialization in vascular graft curgery and is used in conjunction with angiography to administer the angiogenic tRNA synthetase polypeptides or polynucleotides directly to the lumen and wall of the blood vessel
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                                                                             regulating
angiogenesis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 VVKIOKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 415;
                                                                           New human truncated tyrosyl-tRNA synthetase polypeptide for vascular endothelial function, in particular for regulating tumor metastasis and treating myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 2116; DB 4;
; Pred. No. 1.7e-209;
0; Mismatches 0;
                                                                                                                                                     Disclosure; Page 129-30; 150pp; English
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Best Local Similarity 100.
Matches 401; Conservative
                               WPI; 2001-626377/72
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                                               N-PSDB; AAH43604
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AC AAE1
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FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP 121

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Human; tryptophanyl-tRNA synthetase; TrpRS; tyrosyl t-RNA synthetase; TyrRS; vascular endothelial cell function; angiogenesis; wound healing; re-vascularisation; dermal ulcer; pressure sore; venous ulcer; injury; diabetic ulcer; burn; plastic surgery; cosmetic; myocardial infarction; angiography; gene therapy; tumour; inflammation; vascular permeability; rheumatoid arthritis; psoriasis; diabetic retinopathy.
                                                                                                                                                                                                                                                                                        Novel truncated tryptophanyl-tRNA synthetase polypeptides capable of regulating vascular endothelial cell function, preferably angiogenesis, is useful for treating solid tumor or suppressing tumor metastasis in
 Human supermini tryptophanyl t-RNA synthetase in pET20B.
                                                                                                                                                                                                                                                                                                                                              Sxample 1; Page 129-130; 149pp; English.
                                                                                                                                                                                       31-MAR-2000; 2000US-0193471P.
                                                                                                                                                                21-MAR-2001; 2001WO-US008975.
                                                                                                                                                                                                            (SCRI ) SCRIPPS RES INST
                                                                                                                                                                                                                                  Wakasugi K;
                                                                                                                                                                                                                                                        WPI; 2002-010784/01.
                                                                                                                                                                                                                                                                  N-PSDB; AAD22484.
                                                                                                                       WO200175078-A1.
                                                                                                                                                                                                                                  Schimmel P,
                                                                                                 Homo sapiens
                                                                                                                                           11-OCT-2001
                                                                                                                                                                                                                                                                                                                          mammal.
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The patent discloses human aminoacyl tRNA synthetases, particularly truncated tryptophanyl-tRNA synthetases (TrpRS) comprising a Rossmann fold nuclectide binding domain and polynucleotides encoding them. The invention also relates to tyrosyl tRNA synthetases (TyrRS). TrpRS sequences are useful for regulating vascular endothelial cell function, preferably ampiogenesis. Angiogenic TrpRS sequences are useful as wound reating full-thickness wounds (e.g. dermal ulcers, including pressure sores, venous ulcers and diabetic ulcers), burns and injuries. TrpRS sequences can also be used in plastic surgery when reconstruction is required following a burn, other trauma, or even for cosmetic purposes. Angiogenic TrpRS is also used in association with surgery and following the template for communing endothelialisation in vascular graft surgery and for repairing the damage of myocardial infarction and in conjunction with coronary bypass surgery by stimulating the growth of transplanted tissue. TrpRS is also used in conjunction with angiography. TrpRS DNAs are useful in gene therapy. TrpRS antibodies are used in immunoassays to detect the presence of tumours. They are also useful for trensplanted the presence of tumours. They are also useful for blocking endogenous angiogenic activity and retard the growth of solid tumours. These antibodies may also be used to creat inflammation caused by increased vascular permeability. Inhibiting the activity of TrpRS by antisense technology is useful for preventing further growth or even regress solid tumours, and for treating rheumatoid arthrity of TrpRS by such an angiogenesis. The present sequence is human truncated tryptophanyl transplanted to suppermini TrpRS; residues 71-471 of full-length TrpRS. in pET20B protein)

Sequence 415 AA;

ö Gaps ö 100.0%; Score 2116; DB 5; Length 415; 100.0%; Pred. No. 1.7e-209; ive 0; Mismatches 0; Indels 0 Conservative Similarity 401; Query Match Local Matches

1 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH

9 61

FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP 120 ٦

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180
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                                                                                                                                           IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a His6-tagged cleavage product, T1, of recombinant human tryptophany1-tRNA synthase (TrpRS). A related cleavage product, T2, is water soluble and comprises residues 94-471 of full length TrpRS. The water-soluble T2 polypeptide is useful for inhibiting ocular neovascularisation in a patient. The T2 polypeptide is useful for threating neovascular eye diseases, e.g. age-related macular degeneration, coular complications of diabetes, rubecit of plaucoma, retinopathy of prematurity, keratitis, ischaemic retinopathy (e.g. sickle cell),
                                          181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptides derived from human tryptophanyl-tRNA synthase, useful for inhibiting ocular neovascularization in a patient, or for treating neovascular eye diseases, e.g. rubeotic glaucoma, retinopathy, keratitis,
                          LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN
                                                                                                                                                                                                                                   LVIOMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN
                                                                                             VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSPPQIFRDKTDIQCLIPCA
                                                                                                                                                                  IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT
                                                                           VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T2; tryptophanyl-tRNA synthase; TrpRS; ocular neovascularisation; neovascular degeneration; neovascular degeneration; ocular complication; diabetes; rubeotic glaucoma; retinopathy; prematurity; keratitis; ischaemic retinopathy; sickle cell; pathological myopic; ocular histoplasmosis; pterygia; T1; punitate innerchoroidopathy; retinal degeneration; growth factor; vascularisation; vascular endothelial cell function; anglogenesis.
                                                                                                                                                                                                                                                                                 KKALIEVLOPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 401
                                                                                                                                                                                                                                                                                                  KKALIEVLQPLIAEHQARRKEVTDBIVKEFMTPRKLSFDFQ 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        His6-tagged TrpRS Il polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                              240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDODPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
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                                                                                                                                                                                                                                                                                                61 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP 120
                                                                                                                                                                                                                                                                                                                       LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 180
paramotogrean myopic, ocular histoplasmosis, pterygia, or punitate innerchoroidopathy. This polypeptide is particularly useful for treating retinal degeneration to prevent the damaging effects of trophic and growth factors, and for promoting vascularisation to retard retinal degeneration by enhancing blood flow to cells. These are also useful for impliciting vascular endothelial cell function, and in particular, for inhibiting analogement
                                                                                                                                                                                                                                                   VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
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                                                                                                                                                                   Length 415;
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                                                                                                                                                                   100.0%; Score 2116; DB 5; 100.0%; Pred. No. 1.7e-209;
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                                                                                                                                                                                                   Matches 401; Conservative
                                                                                                       inhibiting angiogenesis
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                                                                                                                                    Sequence 415 AA;
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Human; tryptophanyl tRNA synthetase; TrpRS; angiogenesis; cytostatic; vulnerary; Rossmann fold nucleotide binding domain; chemokine; ENAP II; vascular endothelial cell; solid tumour; myocardial infarction; enzyme; endothelial monocyte-activating polypeptide II; tumour metastasis; wound healing; dermal ulcer; endothelialisation; vascular graft surgery;
                                                                                                                                                                            abdominal wound; coronary bypass surgery; gene therapy
                                                                                 Human supermini Tryptophanyl tRNA synthetase/His tag.
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          ABU72386 standard; protein; 415
                                                          (first entry)
                                                                                                                                                                                                       sapiens.
                                                             16-JUN-2003
                                                                                                                                                                                                                     Synthetic.
                                   ABU72386;
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ABU72386
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21-MAR-2001; 2001US-00813718 21-MAR-2001; 2001US-00813718

JS2002182666-A1

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(SCHI/) SCHIMMEL (WAKA/) WAKASUGI

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The invention relates to an isolated polypeptide comprising a truncated tryptophanyl-tENA synthetase (TrpRS) polypeptide comprising a Rossmann fold months of the control o
                                                                                                                                                     New truncated tryptophanyl-tRNA synthetase polypeptide comprising a Rossmann fold nucleotide binding domain or having chemokine activity useful for e.g. for regulating angiogenesis and for treating myocardial
                                                                                                                                                                                                                                                                                                    Example 1; Page 50-51; 91pp; English.
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                          Wakasugi
                                                                            WPI; 2003-340974/32.
N-PSDB; ACA64107.
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                          Schimmel P,
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180 240 300 360 120 181 241 301 KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 361 9 61 LVIQMIDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN VVKIQXHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH ö Length 415; 100.0%; Score 2116; DB 6; 100.0%; Pred. No. 1.7e-209; 0; Mismatches Best Local Similarity 100. Matches 401, Conservative 61 121 122 182 242 ~ 181 241 301 302 62 Query Match 셤 셤 8 셤 ò 셤 ò ద ઠે 셤 ઠે

SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH 83

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The sequences given in AAB47615-18 show full length and truncated versions of trptophanyl-tRNA synthetase (TrpRS). The truncated TrpRS of the invention comprises a Rossmann fold nucleotide binding domain, and is capable of regulating vascular endothelial cell function. It is of the invention comprises a Rossmann fold nucleotide binding domain, and is processed to regulating vascular endothelial cell function. It is of thil length TrpRS with polymorphonuclear leucocyce elastase. Truncated TrpRS is useful for regulating angiogenesis, tumor metastasis, enhancing angiogenesis to a graft, treating myccardial infarction, solid tumor, and condition that would benefit from increased or decreased angiogenesis in a mammal, in particular humans. It is also useful in diagnosis and as a wound healing agent for treating wounds such as dermal ulcers, diabetic concerts, burns and injuries and in plastic surgery when reconstruction is required following a burn or for cosmetic purposes. It is particularly useful in the treatment of abdominal wounds where there is high risk of unfection. Truncated TrpRS promotes endothelialization in vascular graft surgery and is used in conjunction with angiography to administer the anglogenic tRNA synthetase polypeptides or polynucleotides directly to the lumen and wall of the blood vessel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human truncated tyrosyl-tRNA synthetase polypeptide for regulating vascular endothelial function, in particular for regulating angiogenesis, tumor metastasis and treating myocardial infarction.
                                                                                                                                                                                                                                                                                                   Tyrosyl-tRNA synthetase; TyrRS; Rossmann fold nucleotide binding domain; vascular endothelial cell function; burn; plastic surgery; abdomen; polymorphonuclear leucocyte elastase; angiogenesis; tumour metastasis; angiogenesis; graft; myocardial infarction; solid tumour; wound healing; dermal ulcer; diabetic ulcer; endothelialization; tryptophanyl-tRNA synthetase; trpRS; vascular graft surgery.
Disclosure; Page 123-24; 150pp; English.
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                                                                                                                                         AAB47616 Btandard; protein; 437
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                                                                                                                                                                                                                                                               Human mini TrpRS
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VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA 240
                                                                                                                                                                                                        241 IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
                                                                                                                                                                                                                                                                         KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360
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                                         143
                                                                         LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 180
                                                                                          LVIQMIDDEKYLWKDLTLDQAYGDAVGNAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 203
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                                                                                                                                                                                                                           KVNKAPFSGGRDTIEEHROFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, tryptophanyl-tRNA synthetase; TrpRS; tyrosyl t-RNA synthetase; TyrRS; vascular endothelial cell function; angiogenesis; wound healing; re-vascularisation; dermal ulcer; pressure sore; venous ulcer; injury; diabetic ulcer; burn; plastic surgery; cosmetic; myocardial infarction; angiography; gene therapy; tumour; inflammation; vascular permeability; rheumatoid arthritis; psoriasis; diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The patent discloses human aminoacyl tRNA synthetases, particularly truncated tryptophanyl-tRNA synthetases (TrpRS) comprising a Rossmann fold nucleotide binding domain and polynucleotides encoding them. The invention also relates to tyrcosyl t-RNA synthetases (TyrRS). TrpRS sequences are useful for regulating vascular endothelial cell function,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel truncated tryptophanyl-tRNA synthetase polypeptides capable of regulating vascular endothelial cell function, preferably angiogenesis, is useful for treating solid tumor or suppressing tumor metastasis in
                         FIRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP
                                                                                                                                                             VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
          FLRRGI FFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLI PFI FTKWLQDVFNVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human mini tryptophanyl t-RNA synthetase in pET20B.
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N-PSDB; AAD22483.
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al Similarity 100. 401; Conservative

Matches

Query Match Best Local &

100.0%; Score 2116; DB 4; Length 437; 100.0%; Pred. No. 1.8e-209;

punitate innerchoroidopathy, retinal degeneration; growth factor; vascularisation; vascular endothelial cell function; angiogenesis

Schimmel P, Wakasugi K, Friedlander M;

WPI; 2002-698635/75. N-PSDB; ABA00329.

22-FEB-2002; 2002WO-US005185. 23-FEB-2001; 2001US-0270951P. (SCRI ) SCRIPPS RES INST

WO200267970-A1 Homo sapiens.

06-SEP-2002

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preferably angiogenesis. Angiogenic TrpRS sequences are useful as wound healing agents for re-vascularising damaged tissues. They are useful for treating full-thickness wounds (e.g. dermal ulcers; including pressure cores, venous ulcers and diabetic ulcers), burns and injuries. TrpRS sequences can also be used in plastic surgery when reconstruction is required following a burn, other trauma, or even for cosmetic purposes. Angiogenic TrpRS is also used in association with surgery and following the repair of cuts, for promoting endothelialisation in vascular graft conjunction with coronary bypass surgery by stimulating the growth of transplanted tissue. TrpRS is also used in conjunction with angiography. TrpRS DNAs are useful in gene therapy. TrpRS antibodies are used in Transplanted tissue. TrpRS is also used to treat fire also useful for locking endogenous angiogenic activity and retard the growth of solid tumours. These antibodies may also be used to treat inflammation caused by increased vascular permeability. Inhibiting the activity of TrpRS by antisense technology is useful for preventing further growth or even regress solid tumours, and for treating rhemmatoid archritis, psoriasis, diabetic retinopathy, all of which are characterised by abnormal angiogenesis. The present sequence is human truncated tryptophanyl t-RNA angiogenesis.
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This sequence represents a His6-tagged cleavage product, mini-TrpRS, of recombinant human tryptophanyl-tRNA synthase (TrpRS). A related cleavage product, T2, is water soluble and comprises residues 94-471 of full length TrpRS. The water-soluble T2 polypeptide is useful for inhibiting coular neovascularisation in a patient. The T2 polypeptide is useful for treating neovascular eye diseases, e.g. age-related macular degeneration, crematurity, keratitis, ischaemic retinopathy of prematurity, keratitis, ischaemic retinopathy (e.g. sickle cell), pathological myopic, ocular histoplasmosis, pterygia, or punitate innerchoroidopathy. This polypeptide is particularly useful for treating centual degeneration to prevent the damaging effects of trophic and growth factors, and for promoting vascularisation to retard retinal degeneration by enhancing blood flow to cells. These are also useful for intibition or a solution of in particular, for intibition or contact and in particular, for intibition or contact and in particular, for intibition or contact and in particular, for intibition.
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                                                                                                                                                                                                                                                                                                       New polypeptides derived from human tryptophanyl-tRNA synthase, useful for inhibiting ocular neovascularization in a patient, or for treating neovascular eye diseases, e.g. rubeotic glaucoma, retinopathy, keratitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP
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100.0%; Score 2116; DB 5;
Best Local Similarity 100.0%; Pred. No. 1.8e-209;
Matches 401; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Fig 1; 83pp; English.
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T2; tryptophanyl-tRNA synthase; TrpRS; ocular neovascularisation; neovascular eye disease; age-related macular degeneration; ocular complication; diabetes; rubectic glaucoma; retinopathy; prematurity; keratitis; ischaemic retinopathy; sickle cell; pathological myopic; ocular histoplasmosis; pterygia;

His6-tagged mini-TrpRS polypeptide.

(first entry)

10-DEC-2002 AAG79547;

AAG79547 standard; protein; 437

RESULT 8 AAG79547

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26-FEB-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated polypeptide comprising a truncated tryptophanyl-tRNA synthetase (TrpRS) polypeptide comprising a Rossmann Cold mucleotide binding domain or having chemokine activity. The isolated polypeptide is capable of regulating vacaluar endochelial cell function. TyrRS has a C-terminal domain containing an EWAP II (endothelial menocyte activating polypeptide II, a proinflammatory cytokine)-like domain and is similar in sequence to TrpRS. Also included are a polymucleotide containing the TrpRS (or a polymucleotide secondinant vector comprising an isolated TrpRS polymucleotide, a recombinant vector comprising an isolated TrpRS pulsucleotide, a recombinant vector comprising the TrpRS nucleic acid, a recombinant host cell containing the TrpRS nucleic acid and expressing TrpRS, an isolated anticrpRS antibody, producing truncations of TrpRS by treating it with a protease, and suppressing anglogenesis, solid tumours or a condition that would benefit from decreased anglogenesis, solid tumours acondition that would benefit from decreased anglogenesis, solid tumours and condition that composition for transdermal, transmucosal, enteral or parenteral administration. The truncated tRNA synthetase polypeptide is useful for regulating vascular endothelial cell function, particularly for regulating anglogenesis, for treating myocardial infarction and solid tumour, and for suppressing tumour metasteasis.

Anglogenic tRNA synthetase polypeptides are useful as wound healing agents or for treating full thickness wounds such as dermal ulcers, in the promotion of endothelialisation in vascular graft surgery, in the
                                                                                                                                                                                                                                                 Human; tryptophanyl tRNA synthetase; TrpRS; angiogenesis; cytostatic; vulnerary; Rossmann fold nucleotide binding domain; chemokine; EMAP II; vascular endothelial cell; solid tumour; myocardial infarction; enzyme; endothelial moncoyte-activating polypeptide II; tumour metastasis; wound healing; dermal ulcer; endothelialisation; vascular graft surgery; abdominal wound; coronary bypass surgery; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New truncated tryptophanyl-tRNA synthetase polypeptide comprising a Rossmann fold nucleotide binding domain or having chemokine activity useful for e.g. for regulating angiogenesis and for treating myocardial
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                               424
             KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ
                                                                                                                                                                                                                   Human mini Tryptophanyl tRNA synthetase/His tag.
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                                                                                                               ABU72385 standard; protein; 437
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                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                                                                                                                                                                                                                                                                          83
treatment of abdominal wounds where there is a high risk infection, in conjunction with coronary bygass surgery by stimulating the growth of th transplanted tissue, and in gene therapy. The present sequence is a Trp tRNA synthetase protein (full length, truncated or mutant) with a His
                                                                                                                                                                                                                                                                                                                                         84 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKMLQDVFNVP
                                                                                                                                                                                                                                                                24 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH
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                                                                                                                                                                                                                                                                                                                   61 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP
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                                                                                                                                                            Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schoenfeld JR;
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                                                                                                                                                                                               Indels
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                                                                                                                                                        Score 2116; DB 6;
Pred. No. 1.8e-209;
0; Mismatches 0;
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                                                                                                                                                                                               401; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-721702/68
                                                                                                                                                                             Similarity
                                                                                                                      Sequence 437 AA;
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                                                                               affinity tag
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Human tryptophanyl-tRNA synthetase protein.

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into invention retained to nove nuctate acide encouring numbal montain from sectioned and transmembrane proteins. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular corganisms. The fate of many individual cells (for example proliferation, organisms. The fate of many individual cells (for example proliferation, received from other cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic cells enterpetides and hormones) which are received and interpreted by diverse neuropeptides and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention corvides the amino acid sequences of novel human membrane bound receptors and proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a tumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present cells equence of a human properior of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVNKHAFSGGRDTIBEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360
                                                                                                                                                                         This invention relates to novel nucleic acids encoding human PRO secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
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                           New PRO polypeptides, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 2116; DB 7; Length 471; 100.0%; Pred. No. 2.1e-209; ive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 10; SEQ ID NO 250; 918pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 401; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 471 AA;
N-PSDB; ADF76575
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KVNKHAFSGGRDTIBEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIJACGFDINKTFIFSDLDYMGMSSGFYKN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to an adeno-associated viral (AAV) vector comprising a polynucleotide that comprises a nucleic acid segment that encodes a choroidal or ocular neovascularisation inhibitory polypeptide operably linked to a promoter that expresses the segment to produce the polypeptide in a selected mammalian host cell. Such a vector is useful for providing a choroidal or ocular neovascularisation inhibitory polypeptide to a mammal, for use in the therapy of ocular neovascularisation, choroidal neovascularisation, retinal neovascularisation, age-related macular degeneration, visual impairment, ocular dysfunction, loss of vision, retinopathy, or blindness in a human The present sequence is a protein shown in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                     Novel adeno-associated viral vector comprising polynucleotide encoding pigment epithelium-derived factor, useful for treating choroidal neovascularization, blindness, loss of vision.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 LVIQMTDDBEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 FLRRGIFFSHRDMNQVLDAYENKKPPYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH
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                                    Vector; rAAV; recombinant adeno-associated viral vector;
anti-anglogeneels; PEDF; anglogenesis; eye disorder; blindness;
retinal degeneration; macular degeneration; neovascularisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 471;
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100.0%; Pred. No. 2.1e-209;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                            Hauswirth WW, Campochiaro PA, Berns KI;
                                                                                                                                                                                                                                                                                          (UYFL ) UNIV FLORIDA RES FOUND INC. (UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 14; Page 46; Opp; English.
                                                                                                                                                                                                                           20-MAR-2003; 2003WO-US008667.
                                                                                                                                                                                                                                                            20-MAR-2002; 2002US-0366114P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 401; Conservative
                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-779243/73.
N-PSDB; AAL56267.
                                                                                               ophthalmological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 471 AA;
                                                                                                                                                                WO2003080648-A2
                                                                                                                                Homo sapiens
                                                                                                                                                                                             02-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
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120

250

ABU64298 standard; protein; 471 AA

ABU64298

11-MAR-2004 (first entry)

ABU64298;

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Gape

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190

250

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polypeptide of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids polypeptides, antibodies and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistaion syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 VVXIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA 310
                                                                                                                                                                                                                                                                                                                                                                                                     61 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bronchial asthma; chronic obstructive pulmonary disease;
respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLRRGIFFSHRDMQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP
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nucleic acid of the invention; antibodies which specifically bind a
                                                                                                                                                                                                                                                                                   Length 471;
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKALIEVLOPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 471
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100.0%; Pred. No. 2.1e-209;
ive 0; Mismatches 0;
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20-MAR-2003; 2003JP-00077212.
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Matches 401; Conservative
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                                                                                                                                                                                                                                            Sequence 471 AA;
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371 KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to nucleic acids and proteins (ADN38683-ADN40064) whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypoptide of the invention. The invention also relates to expression vectors and host cells comprising a
                                                                                                                                                                                                                                                                                                                                                                       Human; differential expression; cancer; angiogenic disorder; fibrotic disorder; psortiasis; isothemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistation syndrome; scarring; uterine fibroid; detection, diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C286.
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3, Zlotnik
                                                             Gish KC, Gl)
Wilson KE,
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                                                                                                                                                                                              ADN39916 standard; protein; 471
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R, Watson SR,
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21-NOV-2001; 2001US-0332464P.
29-NOV-2001; 2001US-03353439P.
14-DEC-2001; 2001US-0335394P.
14-DEC-2001; 2001US-0343394P.
10-JAN-2002; 2002US-034731P.
10-JAN-2002; 2002US-0347349P.
10-JAN-2002; 2002US-0355250P.
20-FEB-2002; 2002US-0355714P.
29-MAR-2002; 2002US-0368909P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EOSB-) EOS BIOTECHNOLOGY INC
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2002US-0372246P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JUL-2002; 2002US-0397845P.
09-SEP-2002; 2002US-0409450P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-NOV-2002; 2002WO-US036810
                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murray R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-468649/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aziz N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADN39699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003042661-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-APR-2002;
12-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JUL-2002;
22-JUL-2002;
                                                                                                                                                                                                                                                                                     17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAY-2003
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Mack DH,
                                                                                  431
                                                                                                                                                                                                                                         ADN39916;
                                           361
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RESULT 12
ADN39916
ID ADN39916
XX AC ADN39
XX AC ADN39
XX AC ADN39
XX AC ADN39
XX Human
XX Human
XX Human
XX Homo
XX H

471

431 KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ

disease by

Izuhara

Nagai H,

Kubo H,

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The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises

or chronic obstructive pulmonary disease. The method comprises

Ce determining the expression level of a marker gene in a biological sample from a bubject, comparing the expression level a belongical sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13; or (b) a reagent (1) for centing for bronchial asthma or chronic obstructive pulmonary disease; (c) a high induces that induces bronchial asthma in a mouse; (5) a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene or an antisense nucleic acid corresponding to a portion of the marker gene or an antisense nucleic acid corresponding to a portion of the marker gene in and (7) a bnA chip for testing for certivities and can be used in gene therapeutic agent for bronchial asthma or a chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene, and instablmatic activities, and can be used in gene therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, on which a pronchial asthma or chronic obstructive pulmonary disease, on which a pronchial asthma or chronic obstructive pulmonary disease, on which a pronchial asthma or chronic obstructive pulmonary disease. The method for bronchial bething for or screening for a therapeutic 
                                                                                                                                     comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a
                                                                                                                for bronchial asthma or chronic obstructive pulmonary
                                                                                                                                                                                                                                                            Example 11; SEQ ID NO 570; 241pp; English
Үатауа М,
                                                         WPI; 2004-193155/19
                                                                                                                                                                                                           healthy subject.
   z
                                                                                                                      resting
      Ohtani
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Sequence 471 AA;

130 430 240 IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300 KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360 9 71 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH FLRRGI FFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLI PFI FTKWLQDVFNVP LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN **VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA** Gaps ö 100.0%; Score 2116; DB 8; Length 471; 100.0%; Pred. No. 2.1e-209; ive 0; Mismatches 0; Indels 0; 401 KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 401; Conservative Similarity 251 Query Match Best Local S Matches 401 361 61 131 121 191 181 241 301 d q 임 ઠે ď δ g ઠે ò 8

transplant rejection; immune system; rheumatoid arthritis; lupus; inflammatory bowel disease; multiple sclerosis; HIV; AIDS. Morris Ly N, Prentice J, Protein encoded by mRNA of the invention #183. Woodward R, (EXPR-) EXPRESSION DIAGNOSTICS INC. Ź ADP12573 standard; protein; 471 24-APR-2003; 2003WO-US012946. 24-APR-2002; 2002US-00131831. 20-DEC-2002; 2002US-00325899. 12-AUG-2004 (first entry) Wohlgemuth J, Fry K, WO2004042346-A2. Homo sapiens. 21-MAY-2004 ADP12573; RESULT 14 ADP12573 

Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of WPI; 2004-400724/37. the genea

Rosenberg S;

claim 65; SEQ ID NO 2582; 1762pp; English.

The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, as sonotransplant rejection or mechanical organ replacement rejection, in an individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring an individual trovolve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases multiple sclerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a protein that is encoded by the mRNA of the invention.

Sequence 471 AA;

120 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 180 250 9 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP 1 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH Gaps ö Length 471; Indels 100.0%; Score 2116; DB 8; ilarity 100.0%; Pred. No. 2.1e-209; Conservative 0; Mismatches 0; Similarity 401; 61 121 191 71 Query Match Local 중 . 음 à g ò 셤 angiogenic tRNA synthetase polypeptides or polynucleotides directly to the lumen and wall of the blood vessel

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370
                                                                              KVNKHAFSGGRDTIBEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360
                                                                                                                                                                                                                                          Tyrosyl-tRNA synthetase; TyrRS; Rossmann fold nucleotide binding domain; vascular endothelial cell function; burn; plastic surgery; abdomen; polymorphonuclear leucocyte elastase; angiogenesis; tumour metastasis; angiogenesis; graft; myocardial infarction; solid tumour; wound healing; dermal ulcer; diabetic ulcer; endothelialization; tryptophanyl-tRNA synthetase; trpRS; vascular graft surgery.
          IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT
VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
                                  IDODPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT
                                                                                                          401
                                                                                                                  KKALIEVLQPLIAEHQARRKEVTDBIVKEFMTPRKLSFDFQ 471
                                                                                                         KKALIEVLOPLIAEHOARRKEVTDRIVKEFMTPRKLSFDFQ
                                                                                                                                                                     AAB47615 standard; protein; 484 AA
                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                          Human full-length TrpRS.
                                                                                                                                                                                                        07-JAN-2002
                251
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181
                                                  311
                                  241
                                                                     301
                                                                                                        361
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SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH 60

Gaps

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Length 484; Indels

; Score 2116; DB 4;
; Pred. No. 2.1e-209;
0; Mismatches 0;

100.0%; 100.08;

401; Conservative

Query Match Best Local Similarity Sequence 484 AA;

SXXX

Best Loca Matches

8 용 ò

131 FLRRGIFFSHRDMQVLDAYENKKPPYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP 190

FLRRGI FFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLI PFI FTKWLQDVFNVP

61

g

LVIOMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA

121 191 181

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120

180

240

250

251 VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA 310

IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300

241 311 301

IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT

KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360 

KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 401 KKALIEVLOPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 471

371

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361 431

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370

completed: January 10, 2005, 21:19:43 : 157 secs Search cor Job time

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The sequences given in AAB47615-18 show full length and truncated versions of trptophanyl-tRNA synthetase (TrpRS). The truncated TrpRS of the invention comprises a Rossmann fold nucleotide binding domain, and is capable of regulating vascular endothelial cell function. It is of approx. 40 kilo Dalton molecular weight and is produced by cleavage of full length TrpRS with polymorphonuclear leucocyte elastase. Truncated full length TrpRS with polymorphonuclear leucocyte elastasis, enhancing angiogenesis to a graft, treating angiogenesis, tumor metastasis, enhancing angiogenesis to graft, treating myocardial infarction, solid tumor, and a condition that would benefit from increased or decreased angiogenesis in ammmal, in particular humans. It is also useful in diagnosis and as a wound healing agent for treating wounds such as dermal ulcres, diabetic ulcers, burns and injuries and in plastic surgery when reconstruction is required following a burn or for cosmetic purposes. It is particularly cuseful in the treatment of abdominal wounds where there is high risk of infection. Truncated TrpRS promotes endothelialization in vascular graft surgery and is used in conjunction with angiography to administer the

New human truncated tyrosyl-tRNA synthetase polypeptide for regulating vascular endothelial function, in particular for regulating angiogenesis, tumor metastasis and treating myocardial infarction.

31-MAR-2000; 2000US-0193471P. 21-MAR-2001; 2001WO-US008966

WO200174841-A1 Homo sapiens

11-OCT-2001

(SCRI ) SCRIPPS RES INST Schimmel P, Wakasugi K;

WPI; 2001-626377/72. N-PSDB; AAH43602. Disclosure; Page 117-19; 150pp; English

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5.1.6
Compugen Ltd
 GenCore version (c) 1993 - 2005
            Copyright
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protein search, using sw model OM protein Run on:

January 10, 2005, 21:14:03; Search time 40 Seconds (without alignments) 964.573 Million cell updates/sec

2116 1 SNHGPDATEAEEDFVDPWTV......VTDEIVKEFMTPRKLSFDFQ 401 US-09-813-718-10\_COPY\_71\_471 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed sed 0B 0B Minimum I Maximum I Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_79:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	, Length	DB	ΙD	Description
П	2101	99.3	! !	H	A41706	tryptophan-tRNA li
7	2028.5	95.5		н	YWBO	tryptophan-tRNA li
m	1946.5	92.0		Н	YWRBPR	tryptophan-tRNA li
4	1938	91.6		~	S50053	tryptophan-tRNA li
Ŋ	1210	57.2		~	\$58157	hypothetical prote
9	1163	55.0		~	S51901	tryptophan-tRNA li
7	907	42.9		~	C90190	tryptophanyl-tRNA
<b>œ</b>	803	37.5		~	C75020	tryptophany1-tRNA
σ	626.5	29.6		~	G71206	tryptophan-tRNA li
10	534.5	25.3		~	G84373	tryptophanyl-tRNA
11	409.5	19.4		7	F64476	tryptophan-tRNA li
12	397.5	18.8		~	E69131	tryptophan-tRNA li
13	386	18.2		7	T43806	tryptophan-tRNA li
14	370.5	17.5		~	E69461	tryptophanyl-tRNA
15	353	16.		~	D72477	probable tryptopha
16	269.5	12.7		~	F84371	tryptophanyl-tRNA
17	192	9.1		N	H69346	tyrosyl-tRNA synth
18	188	80		7	E72512	probable tyrosyl-t
19	185.5	æ 		7	D95260	tryptophanyl-tRNA
20	185.5	ω.		~	G98125	tryptophan-tRNA li
21	174.5	80		7	B86633	tryptophan-tRNA li
22	172			7	A45999	tyrosine-tRNA liga
23	170.5	8.		~	S75410	
24	169	8		7	H70385	tryptophan-tRNA li
25	167	7.5		~	E75438	tryptophanyl-tRNA
26	166.5	7.9		~	B71496	tryptophan-tRNA li
27		7.8		7	A86410	protein F3M18.22 [
28	63.	7.7		7	E70100	tryptophan-tRNA li
29	163	7.7	460	7	C84750	probable tyrosyl-t

tryptophan-tRNA li	tyrosyl-tRNA synth	tryptophanyl-tRNA	probable tryptopha	tryptophanyl tRNA	tryptophan-tRNA 11	tyrosyl-tRNA synth	probable tyrosine-	tryptophan-tRNA li	tyrosine-tRNA liga	tryptophan-tRNA 11	tyrosine-tRNA liga	tryptophan-tRNA 11	tryptophanyl-tRNA	tryptophan-tRNA li	tryptophan-tRNA li
71300	5072	281654	14994	H86590	72034	84374	03741	54676	71093	11066	59102	72370	82052	73024	WBSF
F7	B7	ဗ	Ĥ	x	U	O	E	ω	Ŀ	∢	Ħ	ပ်	ũ	໙່	⊱
2 F7:	2 B7	2 2	7	7	0	7	C3	3 2	2	2 A	7 H	7	2	8. 2	7
~	375 2 B7	~	~	~	~	~	C)	7	~	~	~	~	2	~	7
337 2 1	7	346 2 (	102 2	344 2	344 2	327 2	408 2	339 2	375 2	337 2	319 2	328 2	365 2 E	343 2 8	328 1 Y
7.5 337 2 1	7.5 375 2 1	346 2 (	7.3 102 2	344 2	7.2 344 2	327 2	7.1 408 2	6.9 339 2	375 2	6.9 337 2	6.5 319 2	6.4 328 2	6.4 365 2 E	6.3 343 2 8	6.2 328 1 Y

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tryptophan-tRNA ligase (EC 6.1.1.2) [similarity] - human N/Alternate names: interferon-inducible protein IPP53; peptide-chain release factor homo

C;Species: Homo sapiens (man) C;Date: 19-May-2000 #sequence

C;Date: 19-May-2000 #sequence revision 19-May-2000 #text change 09-Jul-2004
C;Accession: A41633; A41706; \$19246; JN0676; JH0533; S26287
E;Fleckner, J.; Rasmussen, H.H.; Justesen, J.
Proc. Natl. Acad. Sci. US.A. 89, 11520-11524, 1991
A;Title: Human interferon gamma potently induces the synthesis of a 55-kDa protein (gamm A;Reference number: A41633; MUID:92107982; PMID:1763065

A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mlipe: m

A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-471 <RUB>

A;Cross-references: GB:M77804; NID:g184656; PIDN:AAA67324.1; PID:g184657
R;Buwitt, U.; Flohr, T.; Boettger, B.C.
BRBO J. 11, 489-496; 193
A;Title: Molecular cloning and characterization of an interferon induced human cDNA with A;Reference number: S19246; MUID:92164636; PMID:1537332

A, Accession: S19246

A; Status: preliminary A; Molecule type: mRNA

A; Residues: 1-423, 'R', 425-471 <BUW>
A; Cross-references: EMBL:X62570; NID:g32708; PIDN:CAA44450.1; PID:g32709
A; Note: 213-Ser and 214-Tyr were also found
B; Frolova, L.Y.; Grigorieva, A.Y.; Sudomoina, M.A.; Kisselev, L.L.
Gene 128, 237-245, 1993
A; Title: The human gene encoding tryptophanyl-tRNA synthetase: Interferon-response elemental appropriate to the human gene encoding tryptophanyl-tRNA synthetase: Interferon-response elemental appropriate to the property of the propriate to the property of the

A; Accession: JN0676

A;Molecule type: DNA A;Residues: 1-141;182-471 <FRO1>

A;Cross-references: GB:X67918; GB:S62837; NID:g37968; GB:X67919; NID:g37969; GB:X67920; IN: RD:g37974; GB:X67925; GB:X67926; GB:X679

Rirolova, L.Y.; Sudomoina, M.A.; Grigorieva, A.Y.; Zinovieva, O.L.; Kisselev, L.L. Gene 109, 291-296, 1991
A;Title: Cloning and nucleotide sequence of the structural gene encoding for human tryptoma; A;Reference number: JH0533; MUID:92112058; PMID:1765274
A;Accession: JH0533
A;Molecule type: mRNA

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Gaps

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2028.5; DB 1; No. 4.6e-156;

Score 2028.5; Pred. No. 4.6e 8; Mismatches

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1 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH
                                                                                                                                                                                                                                                                                           FLERGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP
C.Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis
F;24-69/Domain: amino acid-tRNA ligase repeat homology <ATL>
                                                                                                                    95.9%;
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Best Local Similarity 90.8
Matches 364; Conservative
                                                                                                                        Query Match 95.9
Best Local Similarity 95.8
Matches 384; Conservative
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LTYPtophan-TRNA ligase (EC 6.1.1.2) [validated] - bovine

LTYPtophan-TRNA ligase (EC 6.1.1.2) [validated] - bovine

N;Alternate names: tryptophanyl-tRNA synthetase

C;Species: Bos primigenius taurus (Cattle)

C;Accession: A40279; UN054; Sl0460; S14540

R;Garret, M.; Pajor, B.; Trezeguet, V.; Labouesse, J.; Merle, M.; Gandar, J.C.; Benedett

Biochemistry 30, 7809-7817, 1991

A;Title: A mammalian tryptophanyl-tRNA synthetase shows little homology to prokaryotic s

A;Title: A mammalian tryptophanyl-tRNA synthetase shows little homology to prokaryotic s

A;Accession: A40279; MUID:91329348; PMID:1907847

A;Accession: A40279

A;Accession: B40279

A;Accession: B40279

A;Cross-references: UNIPROT:P17248; GB:M74074; EMBL:X53918; NID:g163798; PIDN:AAA30799.1

A;Experimental source: pancreas

A;Experimental source: pancreas

A;Experimental source: pancreas

A;Experimental source: Dancreas

A;Experimental source: Cattle Sequence of several peptides of tryptophanyl-tRNA synthetase from cattle sequence of several peptides of tryptophanyl-tRNA synthetase from cattle sequence of several peptides of tryptophanyl-tRNA synthetase from cattle sequence of several peptides of tryptophanyl-tRNA synthetase from cattle sequence of several peptides of tryptophanyl-tRNA synthetase from Cattle type: protein

A;Fitle: Amino acid sequence of several peptides

A;Fitle: Amino acid sequence

A;Forestsion: JN0354; MUID:90211408; PMID:2631684

A;Forestsion: JN0354; MUID:90211408; PMID:2631684

A;Forestsion: JN0354; MUID:Array

A;Besidues: Li2:124262-287, NV, 288, FF, 289-292, 'Q', 293-294, 'IR';336-353;423-441, 443-449

C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
                             A, Residues: 1-212, 'GD', 215-471 <FRO2>
A; Cross-references: GB:M61715; NID:g340367; PIDN:AAA61298.1; PID:g340368
A; Cross-references: GB:M61715; NID:g340367; PIDN:AAA61298.1; PID:g340368
C; Ganetics:
A; Gene: GDB:WARS; IFP53
A; Cross-references: GDB:119632; OMIM:191050
A; Gene: GDB:WARS; IFP53
A; Introns: 33/3; 105/1; 141/2; 181/2; 242/2; 276/1; 313/3; 371/3; 418/3
A; Introns: 33/3; 105/1; 141/2; 181/2; 181/2; 181/2; 242/2; 276/1; 313/3; 371/3; 418/3
A; Introns: 33/3; 105/1; 141/2; IBI/2; IBI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

99.3%; Score 2101; DB 1;

Best Local Similarity 99.5%; Pred. No. 6.2e-162;

Matches 399; Conservative 0; Mismatches 2;
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tryptophan-tRNA ligase (EC 6.1.1.2) [validated] - rabbit
NyAlternate names: tryptophanyl-tRNA synthetase
NyAlternate names: tryptophanyl-tRNA synthetase
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: 30-Sep-1992 #sequence_revision 13-Feb-1998 #text_change 03-Jun-2002
C;Accession: A33504; 837396
C;Accession: A33504; 837396
C;Accession: N.J.; Marlow, E.; Caskey, C.T.
Proc. Natl. Acad. Sci. U.S.A. 87, 3508-3512, 1990
A;Title: Cloning and expression of a mammalian peptide chain release factor with sequence A;Reference number: A35904; MUID:90239043; PMID:2185472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVIQWTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 180
                                                               240
                                                                                 IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
                                                                                                                                                         374
                                                                                                                                                                                       360
                                                                                                                                                                                                                      434
                   VVKIQXHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
                                                                                                                                            KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL
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                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1946.5; DB 1
Pred. No. 1.9e-149;
1; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complex: homodimer [validated, MUID:94009008]
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90.8%; Pred
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61

241

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uypounction purchan processions Species: Schizosaccharomyces pombe; C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Species: 30-30a-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004 C;Accession: SS8157; T38561
R;Gentles, S.; Churcher, C.M. submitted to the EMBL Data Library, July 1995
A;Reference number: S58145
A;Reference number: S58145
A;Residues: 1-395 <GEN-A;Residues: 1-395 <GEN-A;References: UNIPROT:Q09692; EMBL:Z50142; NID:g1052783; PIDN:CAA90500.1; PID:g105;Reference number: Z21799
A;Reference number: Z21799
A;Residues: 1-395 <GEN-A;Residues: 1-395 <G
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                                                                                                                                                                                                                                                                           196 VIQMSDDEKYLWKDLTLEQAYSYTVENAKDIIACGFDINKTFIFSDLEYMGQSPGFYRNV 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316 DQDPYFRMTRDVAPRIGHPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKSK 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPL 121
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                                                                                                                                                                                                                                                                                                                                                                        VIOMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKNV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 VNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELK 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein SPAC2F7.13c - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                4 EEQIVTPWDVKGSIVDGEEKGIDYERLIVQFGTRKITPEQLERFEKLTGKKPHLLLRRGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTLIDVLQPLIAEHQARRKAVTESTVKEFMTPRQLSFHFQ 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 KALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ
      90.8%; Pred. No. 9.6e-149; ive 21; Mismatches 16;
                                         Conservative
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          Similarity
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S50053
tryptophan-tRNA ligase (EC 6.1.1.2) alpha-2 chain - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S50053; S50052; T49311; S31461; S31462
R;Pajot, B.; Sarger, C.; Bonnet, J.; Garret, M.
J; Mol. Biol. 242, 599-603, 1994
A;Title: An alternative splicing modifies the C-terminal end of tryptophanyl-tRNA synthe A;Reference number: S50052; MulD: 95018226; PMID: 7932716
A;Accession: S50053
A;Molecule type: mRNA
A;Residues: 1-481 cPAJ>
A;Genetics: LSF
A;Note: intron position was determined by sequencing of genomic DNA
A;Genetics: LSF
A;Note: intron position was determined by sequencing of genomic DNA
A;Genetics: S50052
A;Molecule type: mRNA
A;Residues: 1-475 cPAM>
A;Genetics: SF
B;Kisselev, L.L.
B;Genetics: SF
B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AjGene: WRS
AjGene: WRS
Note: clone S5
K) Note: clone S5
C;Superfamily: mammalian tryptophan-tRNA ligase, amino acid-tRNA ligase repeat homology
C;Superfamily: mammalian tryptophan-tRNA aminoacyl-tRNA synthetase; ligase; protein biosynthesi
C;Keywords: alternative splicing, aminoacyl-tRNA synthetase; ligase; protein biosynthesi
F;1-481/Product: tryptophan-tRNA ligase alpha-2 chain long splice form #status predicte
F;1-475/Product: tryptophan-tRNA ligase alpha-2 chain short splice form #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                       240
IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYSSGAMLTGEL 434
                                                                                                                                                                 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360
                                                                                                                                                                                                                                                                                                                                                                                                   VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X69657; NID:g55437; PIDN:CAA49348.1; PID:g55438 A;Genetics: <LSF> A;Gene: WRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 481;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 401
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A;Note: the list of introns may C;Genetics: <SSF>
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tryptophanyl-tRNA synthetase (trpS) [imported] - Sulfolobus solfataricus CiSpecies: Sulfolobus solfataricus CiSpecies: Sulfolobus solfataricus CiSpecies: Sulfolobus solfataricus CiDate: 24-May-2001 #text_change 15-Jun-2001 R.Ary-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001 R.She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-N. Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, Parmett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A.Description: Silfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: trpS
C;Superfamily: mammalían tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126
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                                                                                                                                                        240
                                                                                                                                                                                241 IDODPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
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79 LRKGLFFSERDFTKILDLYEQGKPFFLYTGRGPSSDSMHLGHMIPFVFTKWLQEVPDVPL 138
                                                  122 VIQMTDDEKYLWK-DLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 180
                                                                             KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
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Similarity 48.6%; Pred. No. 1.5e-65;
91; Conservative 68; Mismatches 110; Indels
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A;Accession: C90190
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Best Local Simi
Matches 191;
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A;Status: nucleic acid sequence not shown; translation not shown
A;Status: nucleic acid sequence not shown; translation not shown
A;Status: nucleic acid sequence not shown; translation not shown
A;Nole: L432 <VAW>
A;Cross-references: EMBL:Z48149; NID:g663234; PIDN:CAA88164.1; PID:g663256
A;Nole: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
B;Durand, P.; Hilger, F.; Portetelle, D.; Vandenbol, M.
B;Durand, P.; Hilger, F.; Portetelle, D.; Vandenbol, M.
A;Reference number: S66791
A;Accession: S66793
A;Accession: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSISOI Tryptophan-tRNA ligase (EC 6.1.1.2) [similarity] - yeast (Saccharomyces cerevisiae)
NyAlternate names: protein HRE432; protein 00792; tryptophanyl-tRNA synthetase
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S51901; S56793
R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
submitted to the BMBL Data Library, January 1995
A;Description: Sequence analysis of a 44kb DNA fragment of yeast chromosome XV including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: SGD:WRS1; WRS1; MIPS:YOL097c
A;Cross-references: SGD:S0005457
A;Map position: 15L
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology C;Keywords: ligase
F;117-120/Region: ATP-binding motif (HXGH)
                                                                                                                                                                                                                                                                                        LRRGIFFSHRDMAQVLDAYENKKPFYLYTGRGPSSRAMHVGHLIPFIFTKWLQDVFNVPL 121
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     KHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQDP
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C.Species: Halobacterium sp. NRC-1
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C.Species: Halobacterium sp. NRC-1
C.Date: 02-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 09-Jul-2004
C.Accession: G84373
C.Accession: G84373
C.Species: C.Specie
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                                                this accession replaces an interim accession for a sequence replaced by GenBank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 DPDXTFIFQNSEF----TKIYEMAIPIAKKINFSMAKAVFGFTEQSKIGMIFFPAIQIAP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 GKMSASKPETAIYLTDSPEDVEKKVWKFTLTGGRPTLKEOREKGGEPEKCVVFKWLEIFF 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 EEDDK--KLKERYYACKONGELITGECKRYLISKIOEFLKEHORRRKK-AEKLVEKFKYTG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 GRDVDDFLTAGEQS----IVTGVGPSG-PMHLGHAMVFYFARRLQDEFGARVYVPLSDDE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 DINKTFIFSDLDYMGMSSGFYKNVVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 SFSNSFPQIFRDRTDIQCLIPCALDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQ 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278 TKMSASDPNSSIFLTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFL 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDDDKLEQIRKDY---TSGAMLTGELKKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPR 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 HRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KYLWKDLTLDQAYGDAVE-NAKDIJACGFDINKTFIF---SDLDYM-GMSSGFYKNVVKI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 AEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIFFS
                                            A,Note: this accession replaces an interim accession for a sequence C,Genetics:
A,Gene: PH1921
C,Keywords: aminoacyl-tRNA synthetase, ligase, protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 380;
                                                                                                                                                                                                                                                                Length 301;
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                                                                                                                                                                                                                                                            Query Match 29.6%; Score 626.5; DB 2; Best Local Similarity 44.2%; Pred. No. 5e-43; Matches 134; Conservative 56; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 25.3%; Score 534.5; DB 2; Best Local Similarity 35.4%; Pred. No. 1.9e-35; Matches 141; Conservative 76; Mismatches 140;
             A; Experimental source: strain OT3
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A,Molecule type: DNA
A,Residues: 1-380 <STO>
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G71206
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C.Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C.Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C.Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C.Accession: Genoscope
submitted to the EMBL Data Library, July 1999
A.Accession: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A.Reference number: A75001
A.Status: preliminary
A.Status: preliminary
A.Status: preliminary
A.Residues: 1-385 «KAW>
A.Residues: 1-385 «KAW>
A.Cross-references: UNIPROT:Q9UY11; GB:AJ248288; GB:AL096836; NID:G5458960; PIDN:CAB506
C.Genetics:
A.Status: mental source: strain Orsay
C.Genetics:
A.Gene: trpS; PAB1111
C.Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YLWKD-LTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKNVVKIQKHVT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDY---TSGAMLTGELKKALIE 366
                                                                                                                                                                                                                                                                tryptophanyl-tRNA synthetase (trps) PAB1111 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 EDF-VDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIFFSH 70
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|: | : | |: | |: | |: | 346 IDKLNNFLEEHR-RRREEAKELVHVFKYDGKLA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342 KIQEFLKEHQKRRKKAEKQIEK 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367 VLQPLIAEHQARRKEVTDEIVK 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174
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tryptophan-tRNA ligase (EC 6.1.1.2) [imported] - Encephalitozoon cuniculi (fragment)
C;Species: Encephalitozoon cuniculi
C;Species: Lo-Lan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T41806
R;Peyretaillade, E.; Broussolle, V.; Peyret, P.; Metenier, G.; Gouy, M.; Vivares, C.P.
Mol. Biol. Evol. 15, 683-889, 1998
A;Tit.le: Microsporidia, anitochondrial protists, possess a 70-kDa heat shock protein gens A;Reference number: Z22693; MUID:98277683; PMID:9615449
A;Accession: T43806
A;Accession: T43806
A;Status: preliminary; translated from GB/EMBL/DDBJ
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N.Alternate names: tryptophanyl-tRNA synthetase
C, Species: Methanococcus jannaschii
C, Species: Methanococcus jannaschii
C, Species: Nethanococcus jannaschii
C, Species: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C, Accession: F64476
C, Mccession: F64476
A, Mitcher C, Julian, M.C.; Cotton, M.D.; Roberts, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A, Mitcher Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A, Reference number: A64300; MUID:96337999; PMID:8688087
A, Status: preliminary; nucleic acid sequence not shown; translation not shown
A, Residues: 1-370 - RUL.
A, Residues: 1-370 - RUL.
A, Residues: 1-370 - RUL.
A, Cross-references: UNIPROT:058810; GB:U67582; GB:L77117; NID:g1592064; PIDN:AAB99425.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Stārt codon: GTG
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIMSFETTKELALNEYITNYIALGLDPEKINVYLQSKYQKV-----KDLALILSKRTNWS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRT--DIQCLIPCAIDQDPYFRM 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KDLTLDQAYGDAV-ENAKDIIACGPDINKTFIFSDLDYMGMSSGFYKNVVKI-QKHVTFN 191
                                      213
                                                                                                            NKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDD-KLEQIRKDYTSGAMLTGELK 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 PWIVQISSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIFFSHRDMNQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 pw--ETPAV--iDYKKTMEQFGVKPIVDVLGDLKEE-----HHFFRRNIILGHRDFERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRDVAPR---IGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKHA
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                       PYFRMTRDVAPRIGYP - - KPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKV
QKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQD
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                                                                                                                                                                                                                                                 KALIEVLOPLIAEHQARRKEVTDEIVKEFMTPRKLSFD 399
                                                                                                                                                                                                                                                                          Query Match 19.4%; Score 409.5; DB 2; Best Local Similarity 30.9%; Pred. No. 2.3e-25; Matches 119; Conservative 72; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 AYERVVEFLKDLKEKREQAKEIAVK 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: FOR1375885-1376997
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tryptophan-tRNA ligase (EC 6.1.1.2) - Methanobacterium thermoautotrophicum (strain Delta NyAlternate names: tryptophanyl-tRNA synthetase (Species: Methanobacterium thermoautotrophicum (5)Species: Methanobacterium thermoautotrophicum (5)Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004 (C)Accession: E69131 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; I R;Smith, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Ghbon, R.; Jiwani, N.; Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1397 A;Tile: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct: A;Reference number: A69000; MUID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:026352; GB:AE000812; GB:AE000666; NID:92621298; PIDN:AAB8475:
A;Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Start codon: TTG
C; Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
C; Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
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18.8%; Score 397.5; DB 2;
Best Local Similarity 27.9%; Pred. No. 2.1e-24;
Matches 107; Conservative 76; Mismatches 153;
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A; Residues: 1-364 <MTH>
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A;Gene: MTH251
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Search completed: January 10, 2005, 21:23:46 Job time : 42 secs
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C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Accession: E69461
R;KLenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
S;Richnan, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A;Recession: E69461
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1.420 <cLEs
A;Cross-references: UNIPROT:028579; GB:AE000986; GB:AE000782; NID:g2689309; PIDN:AAB8955
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
A;Residues: 1-134 <PEY>
A;Cross-references: UNIPROT:O96771; EMBL:AJ012470; PIDN:CAA10034.1
C;Superfamilian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
C;Keywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSHRDMNQVLDAYENKKPFYLYTGRGPSSBAMHVGHLIPFIFTKWLQDVFNVPLVIQMTD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKYLWK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |::: | ||| || ::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |:: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |:: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |:: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |:: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKNVV-KIQKHVTFNQV 193
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                                                                                                                                                                                                                                                                                                                                                                                  | : | | : | : | : | : | : | | | | EQRITPWDVEVVSTDEVPVAIDYDKIINQFGCEKFNQALADRLEKLSGKPAHYFFRRGIV 62
                                                                                                                                                                                                                                                                                                                                        12 EDFVDPWTVQTSSAK----GIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIF 67
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                                                                                                                                                                                             Length 134;
                                                                                                                                                                                     ch 18.2%; Score 386; DB 2; Length 13. Similarity 51.5%; Pred. No. 4.4e-24; 68; Conservative 25; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 17.5%; Score 370.5; DB 2; Length 9 Best Local Similarity 27.3%; Pred. No. 3.9e-22; Matches 118; Conservative 60; Mismatches 166; Indels
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DEKFLWKSMRLE 134
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Best Local S
Matches 68
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C;Accession: D72477

C;Accession: D72477

Swavabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahi awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ki DNA Res. 6, 83-101, 1999

A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrn A;Reference number: A72450; MUID:99310339; PMID:10382966

A;Accession: D72477
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A;Experimental source: strain Kl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQ-DVFNVPLVIQMTDDEKYLW 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 RDLADRMAGVVELERPASTYHKLQPGLDG--RKMSSSRPDSTIFLTDPPEVARNKIFR-A 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KDLTLDQAYGDAVEN-AKDIJACGFDINKT-FIFSDLDYMGMSSGFYKNVVKIQKHVTFN 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 VDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIFFSHRDMN 74
                                                                                                                                                                                                                                                                                                                                               probable tryptophanyl-tRNA synthetase APE2461 - Aeropyrum pernix (strain Kl)
                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 16.7%; Score 353; DB 2; Length 374; Best Local Similarity 30.4%; Pred. No. 8.7e-21; Matches 119; Conservative 70; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 ALIEVLOPLIAEHQARRKEVTDEIVKEFMTPR 394
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                                                                        370 PLIAEHQARRKEV 382
                                                                                                                                                 SFLKEHQEKMEAV 411
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O70184 cavia porce
Q7q9d2 anopheles g
Q7q0h6 anopheles g
Q9u4y0 drosophila
Q9u4y1 drosophila
Q9v4g2 drosophila
Q9v1z2 caenorhabdi
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Q6fqb6
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Q12109
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                  1825181 segs, 575374646 residues
                                                                            US-09-813-718-10_COPY_71_471
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Q994X0
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1164.5
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Aas52037 ashbya go Q8idw3 plasmodium Q7rb96 plasmodium Q8sy5 encephalito Q7f017 giardia lam Q976m1 sulfolobus Q97xx0 sulfolobus Q91x1 pyrococcus Q9uy11 pyrococcus Q9uy15 leishmania Q8rtu5 pyrobaculum Q74mk6 nanoarcha	
AASS2037 081DW3 07RB96 07RB96 0850Y5 07R0U7 SYW_SULPO SYW_EULSO SYW_PYRFU SYW_PYRFU SYW_PYRFU SYW_PYRFU SYW_PYRRO SYW_PYRRO OUTF5 074MK6 AAR38970	ALIGNMENTS
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6426 6832 6832 4853 386 386 3365 345 377 377	
04444446000000000000000000000000000000	
1154.5 1026 998 942 916 916.5 803 795.5 701	
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MEDLINE=92164636; PubMed=1537332;
Buwitt U., Flohr T., Boettger B.C.;
"Molecular cloning and obsracterization of an interferon induced human
"Molecular cloning and obsracterization of an interferon induced human
cDNA with sequence homology to a mammalian peptide chain release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-92105071; PubMed-1761529;
Rubin B.Y., Anderson S.L., Xing L., Powell R.J., Tate W.P.,;
"Interferon induces tryptophanyl-tRNA synthetase expression in human
fibroblasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92112058; PubMed=1765274; Frolova A.Y., Zinovieva O.L., Frolova L.Y., Sudomoina M.A., Grigorieva A.Y., Zinovieva O.L., Kisselev L.L.; "Cloning and nucleotide sequence of the structural gene encoding for human tryptophanyl-tRNA synthetase."; Gene 109:291-296(1991).
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"Human interferon gamma potently induces the synthesis of a 55-kDa
protein (gamma 2) highly homologous to rabbit peptide chain release
factor and bovine tryptoplanyl-tRNA synthetase."
Proc. Natl. Acad. Sci. U.S.A. 88:11520-11524(1991).
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
SYW HUMAN STANDARD; PRT; 471 AA.
P233B1; P7855; Q9UDL3;
01-NOV-1991 (Rel. 20, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase)
(TrpRS) (IFP53) (hWRS).
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. 266:24245-24248(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92107982; PubMed=1763065;
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EMBO J. 11:489-496(1992)
                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lux , Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Schmutz J., Myers R.M., Schhall J.E., Schmutz J., Myers R.M., Schhall J.E., Schmerch A., Schalk J.E., Schmerch A., Schalk J.E., Jones S.J.M., Marza M.A., Schall J.E., Jones S.J.M., Marza M.A., Schall J.E., Jones S.J.M., Marza M.A., Schall J.E., Jones B.J.M., Marza M.A., Schall J.B., Jones B.J.M., Marza M.A., Schall J.B., Jones B.J.M., Marza M.A., Schall J.B., 1911-length human M.M.
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-13 FROM N.A. MEDIAGES, MEDIAGES 1.V., Narovliands A.M., Turpaev K.T.; SOKOLOVA I.V., Narovliandski, A.N., Amchenkova A.M., Turpaev K.T.; "Alternative splicing of 5'-terminal exons of the human tryptophanyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE-9225128; PubMed=1373391;

Bange F.-C., Flohr T., Buwitt U., Boettger E.C.;

"An interferon-induced protein with release factor activity is a tryptophanyl-trNA synthetase."

I-CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).

SUBUNIT: Homodimer to an an animacyl-tRNA synthetase family.

I-SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.

SIMILARITY: Contains I WHEP-TRS domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-533292; PubMed=7685728; Frolova L.Y., Grigorieva A.Y., Sudomoina M.A., Kisselev L.L.; Frolova L.Y., Grigorieva A.Y., Sudomoina M.A., Kisselev L.L.; The human gene encoding tryptophanyl-tRNA synthetase: interferonresponse elements and exon-intron organization."; Gene 128:237-245(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microsequences of 145 proteins recorded in the two-dimensional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E., Vandekerckhove J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein database of normal human epidermal keratinocytes.";
Electrophoresis 13:960-969(1992).
                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 265-276; 278-296; 299-317 AND 350-365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-141 AND 182-471 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   tRNA synthetase gene.";
Mol. Biol. (Mosk.) 30:319-329(1996).
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BC017489; AAH17489.1; -...
S82905; AAB39381.1; -...
K67920; CAB94198.1; -...
K67921; CAB94198.1; JOINED.
K67923; CAB94199.1; JOINED.
K67923; CAB94199.1; JOINED.
K67924; CAB94199.1; JOINED.
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MEDLINE=93162043; PubMed=1286667;
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EMBL; X59892; CAA42545.1; -.
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71 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH 130
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                                                                                                                                                                                                                                                                                                                                                                                                R Genew; HGNC::.....

R MIM; 191050; ...

R GO; GO:0005625; C:soluble fraction; TAS.

R GO; GO:0005625; C:soluble fraction; TAS.

R GO; GO:0006412; P:protein biosynthesis; TAS.

DR GO; GO:0006412; P:protein biosynthesis; TAS.

DR GO; GO:0006436; P::ryptophanyl-tRNA aminoacylation; TAS.

DR HICEPTO; IPRO01305; TRNA-synt_1b.

DR InterPro; IPRO01305; TRNA-synt_1b.

DR InterPro; IPRO01315; TRNA-synt_1b.

DR InterPro; IPRO01315; TRNA-synt_1b.

DR Fam; PF00458; WHEP-TRS; ...

DR PRINT; PRO0159; TRNA-Synt_1b; 1.

DR PRINT; PRO0179; TRNA-Synt_1b; 1.

DR PRINT; PRO0178; AA TRNA LIGASE I; 1.

DR PROSITE; PS00178; AA TRNA LIGASE I; 1.

DR PROSITE; PS00178; AA TRNA LIGASE I; 1.

DR PROSITE; PS00178; AA TRNA Synthetase; ATP-binding;

XW 3D-structure; Aminoacy1-tRNA synthetase;

COTAL COTAL REGION COTAL REGION IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TEACH IN TE
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"KMSKS" region.

SY -> GD (in Ref. 3).

A -> R (in Ref. 4).

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                         EMBL; X67927; CAB94199.1; JOINED.
BMBL; X67928; CAB94199.1; JOINED.
PIR; A1633; A41706.
PDB; 1R6T; X-ray; A/B=1-471.
PDB; 1R6T; X-ray; A/B=4-471.
PDB; 1UH; X-ray; A/B=8-471.
Aarhus/Ghent-2DPAGE; 3524; IEF.
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Genew; HGNC:12729; WARS.
MIM; 191050; -.
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353
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Best Local Similarity
Matches 399; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGEGLDATEADEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELVNRIERATGQRPHR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 FLRRGIFFSHRDMHQILDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP 195
                                                     MEDLINE=91329348; PubMed=1907847;
Garret M., Pajot B., Trezeguet V., Labouesse J., Merle M.,
Gandar J.-C., Benedetto J.-P., Sallafranque M.-L., Alterio J.,
Gueguen M., Sarger C., Labouesse B., Bonnet J.;
"A mammalian tryptophanyl-tRNA synthetase shows little homology to
prokaryotic synthetases but near identity with mammalian peptide chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP
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                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).
-!- SUBUNIT: Homodimer.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
-!- SIMILARITY: Contains 1 WHEP-TRS domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISPENSABLE TO THE CATALYTIC ACITVITY.
"HIGH" region.
"KNSKS" region.
L -> M (in Ref. 2).
F7E531750137E832 CRC64;
                                                                                                                                                                                                                                                         Garret M., Trezeguet V., Pajot B., Gandar J.-C., Merle M.,
Guegueiv M., Benedetto J.-P., Sarger C., Alteriot J., la Bouessec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 475;
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                                                                                                                                                                                                                                                                                           Labouesse J., Bonnet J.;
Submitted (MAR-1990) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) =
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llarity 95.8%; Pred. No. 3.6e-154;
Conservative 8; Mismatches 8;
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InterPro; IPR009068; S15/NS1 bind.

InterPro; IPR001305; ENRA-synt_1b.

InterPro; IPR001305; ENRA-synt_1b.

InterPro; IPR001305; TRP_ERNA-synt_1.

InterPro; IPR001305; TRP_ERNA-synt_1b.

InterPro; IPR001305; TRNA-synt_1b.

Pfam; PF00579; TRNA-synt_1b; 1.

Pfam; PF00159; TRNA-synt_1b; 1.

PRINTS; PR01039; TRNA-SYNTHTRP.

TIGREAMS; TIGR00233; trp5; 1.

PROSITE; PS00762; WHEP-TRS; 1.

PROSITE; PS00762; WHEP-TRS; 1.

Aminoacy1-tRNA synthetase; ATP-binding; bi:
                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WHEP-TRS
                                                                                                                                                                                     Biochemistry 30:7809-7817(1991).
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53729 MW;
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DOMAIN 24 69

DOMAIN 1 117
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                                                                                                                                                                                                                       SEQUENCE OF 17-475 FROM N.A.
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178
357
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353 3
17
475 AA;
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les 384; Conserv
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                                                                                                                                                                                                                                           TISSUE=Pancreas;
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVIQMTDDEKYLWKDLTLDQAYSYAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
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p17248;
01-AUG-1990 (Rel. 15, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
05-MJL-2004 (Rel. 44, Last annotation update)
Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
                                                                                                               Plasmid pCNVSPORT 6.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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                            02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Human full-length cDNA clone CSODMO04YH09 of Fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                               Li W.B., Gruber C., Jessee J., Polayes D.;
"Full-length cDNA libraries and normalization.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX248006; CAD62335.1; -.
                                                                                                                                                                                                                                         Genoscope;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                  471 AA; 53165 MW; E96344449053A0D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.3%; Score 2101; DB 2;
99.5%; Pred. No. 5.4e-160;
iive 0; Mismatches 2;
                 Created)
                02-MAR-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.5
Matches 399; Conservative
                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                          TISSUE=Fetal liver;
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                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                sapiens (human)
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Query Match
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Q9DC65;
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                                                                IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
                                                                                                                              KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360
                                                                                                                                                 KVNKAAFSGGRDTVEEHRQFGGNCDVDVSFMYLTFFLBDDDKLEQIRRDYTSGAMLTGEL 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94009008; PubMed=8404867; PubLines=94009008; PubMed=8404867; Prolova L.Y., Dalphin M.E., Justessen J., Powell R.J., Drugeon G., McCaudana K.K., Kisselav L.L., Tate W.P., Haenni A.-L.; Mammalian polypeptide chain release factor and tryptophanyl-tRNA synthetase are distinct proteins."; EMBO J. 12:4013-4019(1933).

-!- CATALYIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).

-!- SIMILARITY: Belongs to class: I aminoacyl-tRNA synthetase family.
-!- SIMILARITY: Contains I WHEP-RS domain.
-!- CAUTION: Was originally (Ref.1) thought to be a eukaryotic release.
                  VVKI OKHVTFNOVKGI FGFTDSDCIGKI SFPAIOAAPSFSNSFPOI FRDRIDVQCLIPCA
                                                                                  WKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90239043; PubMed=2185472; MEDLINE=90239043; PubMed=2185472; Lee C.C., Craigen W.J., Muzny D.M., Harlow E., Caskey C.T.; Lee C.C., craigen W.J., amammalian peptide chain release factor "Cloning and expression of a mammalian peptide chain release factor "Cloning and expression of tryptophanyl-tRNA synthetases.";
                                                                                                                                                                                                                                                                                                          SYW RABIT STANDARD; PRT; 475 AA.
P23512; Q28607;
01-NOV-1991 (Rel. 20, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                               KKELIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSYDFQ 475
                                                                                                                                                                                            KKALIEVLOPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        with sequence similarity to tryptophanyl-tRNA sy
Proc. Natl. Acad. Sci. U.S.A. 87:3508-3512(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REVISIONS TO 169-174 AND 227-228, AND FUNCTION
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InterPro; IPR002305; IRNA-8ynt_1b.
InterPro; IPR001412; IRNA-8ynt_I.
InterPro; IPR002306; Trp_IRNA-8ynt_I.
InterPro; IPR007308; WHEE-TRN.
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EMBL; U02595; AAB60257.1; -.
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 181
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Pfam; PF00579; tRNA-synt 1b; 1. Pfam; PF00458; WHEP-TRS; 1. PRINTS; PR01039; TRNASYNTHTRP.

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254
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                                                                                                                                                                                                                                                                                                   SHGDPEAVDDKEDFVDPWTVRTSSAKGIDYDKLIVQFGSSKIDKELVNRIERATGQRPHR 134
                                                                                                                                                                                                                                                                                                                                                             FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP 120
                                                                                                                                                                                                                                                                                                                                                                                       VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255 VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFHGQADIQCLIPCA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      315 IDQDPYFRMTRDVAFRIGYFRPALLHSTFFFALQGAQTKMSASDPNSSIFLTDTAKQIKT 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360
                                                                                                                                                                                                                                                                                                                                                                                                                                              121 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYSSGAMLTGEL 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last amountation update)
Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
clone:1200002C07 product:tryptophanyl-tRNA synthetase, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 NHG-PDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 IDODPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT
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TIGRPAMB; TIGRO0233; trpS; 1.
PROSITE; PS00178; AA TRNA LIGASE_I; 1.
PROSITE; PS00178; WHEP_TRS; 1.
PROSITE; PS00762; WHEP_TRS; 1.
Aminoacyl-trnA synthetage; ATP-binding; Ligase; Protein biosynthesis.
DOMAIN 23 68 WHEP-TRS.
                                                                                                                                                                                                                                      Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                        DB 1; Length
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                                                                                  23 68 WHEP-TRS.
168 177 "HIGH" region.
353 357 "KWSKS" region.
475 AA; 53799 WW; 33BC9E718FF45DC4 CRC64;
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                                                                                                                                                                                                                                        13;
                                                                                                                                                                                      92.7%; Score 1961.5; DB 1; 91.5%; Pred. No. 8.6e-149; iive 20; Mismatches 13;
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STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=21085660; PubMed=11217851;
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                                                                                                                                                                                                                                      Conservative
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VIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKNV 181

122 196 182 256 242 316 302

VKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAI 241

VKIQKHVTFNQVKGIFGFTDSDCIGKISFPAVQAAPSFSNSFPKIFRDRTDIQCLIPCAI

315

DODPYFRWIRDVAPRIGHPKPALLHSTFFPALQGAQIKWSASDPNSSIFLIDIAKQIKSK 375

DODDYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTK 301

436 KTLIDVLQPLIAEHQARRKAVTEETVKEFMTPRQLSFHFQ 475 KALIEVLOPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 401

362

VNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELK 361

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A Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Horri F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Muramatsu M., Hayashizaki Y.,
L Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
R EMBL, AKO04541; BAB233571; -.
                                 the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                             SEQUENCE FROM N.A.
STRAALN=CS7BL/6J; TISSUB=Lung;
STRAALN=CS7BL/6J; TISSUB=Lung;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subbraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630 (2000).
                                                                                                                                                                                                                                                                                                                       STRAIN-CSTBL/60; TISSUE-Lung;
MEDLINE-2050913; PubMed-11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
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GG; GG:0005524; F:ATP binding; IEA.
GG; GG:0004830; F:tryptophan-tRNA ligase activity; IEA.
GG; GG:0006436; F:tryptophanyl-tRNA aminoacylation; IEA.
InterPro; IPR003068; S15/NS1 bind.
InterPro; IPR00305; tRNA-synt_1b.
InterPro; IPR001412; tRNA-synt_1.
InterPro; IPR002306; Trp_ERNA-synt_1b.
InterPro; IPR002306; Trp_ERNA-synt_1b.
InterPro; IPR00579; WHEP-TRS.
Pfam; PF00579; WHEP-TRS.
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TIGRFAMS; TIGR00233; trps; 1.
PROSITE; PS00178; AA TRNA LIGASE I; 1.
PROSITE; PS00762; WHEP TRS; 1.
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 STRAIN=C57BL/6J; TISSUE=Lung;
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les 366; Conservative
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TRAIN-EMERITY TISSUE-Mammary tumor. WAP-Tag model. 5 months old;

KE STRAIN-EMERITY TISSUE-Mammary tumor. WAP-Tag model. 5 months old;

KIAUSE-22388257; PubMed=12477932;

RA Strausberg R.L., Feathgold B.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Bromstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glubs R.A.,

Rahey J., Helton E., Ketteman M., Rodan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Nara M., Green E.D., Dickson M.C.,

Radriguez A.C., Grimwood J., Schwutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.;

A Jones S.J., Marra M.A.;

RA Generation and initial analysis of more than 15,000 full-length human and mouse cDNs sequences."
                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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STRAIN=NWRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004830; F:LYTypcophan-tRNA ligase activity; IEA.
GO; GO:0006436; P:LYTypcophanyl-tRNA aminoacylation; IEA.
InterPro; IPR009068; S15/NS1_bind.
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                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                  Tryptophanyl-tRNA synthetase.
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Submitted (FEB-2001) to the
EMBL; BC003450; AAH03450.1;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
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62 LRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPL 121

NHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHF

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Matches

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RESULT 8
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ID SYW MOUSE
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DT 01-OCT-1993 (
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STRAIN-C57BL/6; TISSUE-Brain;
STRAIN-C57BL/6; TISSUE-Brain;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Brownstein M.J., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                        NHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHF
                                                                                                                                                                                                                                                        LRRGI FFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLI PFI FTKWLQDVFNVPL
                                                                                                                                                                                  Gaps
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Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                        Query Match 92.5%; Score 1957; DB 2; Length 481; Best Local Similarity 91.5%; Pred. No. 2e-148; Matches 366; Conservative 20; Mismatches 14; Indels
                                                                                                                                    54325 MW; A754E1DDF58E2EF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KALIEVLOPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ
InterPro; IPR002305; tRNA-synt_1b.
InterPro; IPR001412; tRNA-synt_1.
InterPro; IPR002306; Trp_tRNA-synt_1b.
InterPro; IPR000738; WHEP-TRS.
Pfam; PF00459; WHEP-TRS; 1.
Pfam; PF00458; WHEP-TRS; 1.
PRINTS; PR01039; TRNASTNTHTR.
TIGRRAMs; TIGR00233; trpS; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_1; 1.
PROSITE; PS0076; WHEP_TRS; 1.
PROSITE; PS0076; WHEP_TRS; 1.
PROSITE; PS0076; WHEP-TRS; 1.
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Name=Wars;
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Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 VIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 NHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHF
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                                                                                                                                                                                                                                                                                                                                                                                  Strauberg R.;
Strauberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; BC046522; AAH46232.1; -.
HSSP; PC07844; FYYJ.
MGD; MGI:104630; Wars.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0006436; F:ATP binding; IEA.
InterPro; IPR00306; SIS/NN1_bind.
InterPro; IPR00306; TRNA-synt_1.
InterPro; IPR00306; TRD tRNA-synt_1.
InterPro; IPR00306; TRD tRNA-synt_1.
InterPro; IPR00308; MHEP-TRS.
Pfam; PF00459; WHEP-TRS; 1.
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                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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(Rel. 27, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO1039; TRNASYNTHTR.
TIGRFAMS; TIGR00233; trps; 1.
PROSITE; PS00178; AR TRNA LIGASE I; 1.
PROSITE; PS00762; WHEP TRS; 1.
SEQUENCE 475 AA; 53613 MW; D841D8B5
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 92.3%;
Best Local Similarity 91.2%;
Matches 365; Conservative
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*** ALSOURE-2738825; PubMed=12477932; Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Straubberg R.L., Feingold E.A., Grouse L.H., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., A Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J., Raka S.S., McEwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H., A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Sanchez A., A Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Xi Texpwinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., And Manne A., Ander A., Shalska U., Smailus D.E., Schnerch A., Schein J.E., Ander A., Ander A
                                     DODPYFRMTRDVAPRIGHPKPALLHSTFPPALQGAQTKMSASDPNSSIFLTDTAKQIKSK 375
                                                                                                                                                                                                                                                                                                242 DQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTK 301
                                                                                                                                                                                                                                                                        VNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELK 361
                                                                                                                            VIOMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKNV
                                                                                                   VKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klein S.L., Strausberg R.L., Wagner L., Pontlus J., Clifton S.W., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                       KALIEVLOPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 401
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dev. Dyn. 225:384-391(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mouse cDNA sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klein S., Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=MGC81110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LISSUE=Ovary
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R MGD; MGI: J04630; Wars.

R InterPro; JPR002306; ENA-synt_lb.

R InterPro; JPR002306; TRNA-synt_lb.

R InterPro; JPR002306; Trp LRNA-synt_lb.

R InterPro; JPR000738; WHEP-TRS;

R Pfam; PF00459; RNA-synt_lb; 1.

Pfam; PF00459; WHEP-TRS; 1.

PR MINTS; PR01039; TRNA-SYNTHTRP.

R PRINTS; PR01039; TRNA-SYNTHTRP.

R PROSITE; PS00176; MHEP TRS; 1.

R PROSITE; PS00176; WHEP TRS; 1.

R PROSITE; PS00176; WHEP TRS; 1.

R Alternative splicing; Aminoacyl-tRNA synthetase; ATP-binding; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 NCDSDATKASEDFVDPWTVRTSSAKGIDYDKLIVQPGSSKIDKELINRIERATGQRPHRP 135
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                                                                                                                                                                                                          MEDLINE=95018226; PubMed=7932716;
Pajot B., Sarger C., Bonnet J., Garret M.;
Pajot B., Sarger C., Bonnet J., Garret M.;
An alternative splicing modifies the C-terminal end of tryptophanyl-
tRNA synthetase in murine embryonic stem cells.";
J. Mol. Biol. 242:599-603(1994).
-!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +
diphosphate + L-tryptophanyl-tRNA(Trp).
-!- SUBUNIT: Homodimer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       found only in embryonic stem cells. SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family. SIMILARITY: Contains 1 WHEP-TRS domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P32921-1; Sequence=Displayed;
Name=-5, Synonyme=Short;
IsoId=P32921-2; Sequence=VSP 006313;
TISSUE SPECIFICITY: Isoform 2 is widely expressed, isoform 1 is
05-JUL-2004 (Rel. 44, Last annotation update)
Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
                                                                                  Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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"KMSKS" region.
Missing (in isoform 2).
/FTId=VSP_006313.
                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=Long;
                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
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EMBL; X69657; CAA49348.1; -.
PIR; S50053; S50053.
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Best Local Similarity 90.8
Matches 363; Conservative
                                                              Name=Wars; Synonyms=WRS;
                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
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Kenopus laevis (African clawed frog).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Barrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    research: The NIH Xenopus
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                                                                                                                                                                                                                                                                                                       Length 475;
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  (APR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                             761EF9EA4B754F71 CRC64;
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14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.1%; Score 1844; DB 2;
83.8%; Pred. No. 2.3e-139;
ive 44; Mismatches 21;
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                "Genetic and genomic tools for Xenopus
                                                                                                                                                                          PRINTS; PRO1039; TRNASYNTHTRP.
TIGRRAMS; TIGRO0233; LTDS; 1.
PROSITE; PSO0178; AA_TRNA_LIGASE_I; 1.
PROSITE; PS00762; WHEP_TRS; 1.
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53856 MW;
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Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                     Best Local Similarity 83.8
Matches 335, Conservative
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SEQUENCE FROM N.A.
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AAH68695;
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Klausner R.D., Celling F.S., Wagner L.H., Derge J.G.,
Altausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul R.F., Jordan H., Moore T., Max S.I., Wang J., Hsheh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Socres M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan R.J., Malke J.A., Gunazane P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         435
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Klein S., Strausberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC06869. AA46695.1; -.
Hypothetical protein.
SEQUENCE 475 AA, 53856 MW; 761EF9EA4B754F71 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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83.8%; Pred. No. 2.3e-139;
tive 44; Mismatches 21;
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Conservative 4
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05-JUL-2004 (TrEMBLrel. 27,
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05-JUL-2004 (TrEMBLrel. 27,
Hypothetical protein.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.
                                                                                                                                                                                   PRELIMINARY;
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SEQUENCE 379 AA;
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                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                        Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                         Genetic and genomic tools for Xenopus research: The NIH Xenopus
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Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 475;
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                                                                                                                                                                                                                                                                                                                                           Klein S., Strausberg R.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO46713; AAH46713.1; -.
HSSB; P07814; 1FYJ.
                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004830; F:tryptophan-tRNA ligase activity; IEA.
GO; GO:0006436; P:tryptophanyl-tRNA aminoacylation; IEA.
InterPro; IPR002068; S15/S1 bind.
InterPro; IPR002305; tRNA-Synt_1b.
InterPro; IPR001412; tRNA-Synt_1.
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PRINTS; PR01039; TRNASYNTHTRP.
TIGREMAS; TIGR00233; LTDS; LTDS; LTDS;
PROSITE; PS00178; AA TRNA LIGASE I; 1.
PROSITE; PS00762; WHEP TRS; 1.
PROSITE; PS00762; WHEP TRS; 1.
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; Pred. No. 2e-137;
39; Mismatches 2
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InterPro; IPR000738; WHED-TRS.
                                                                                                                                                                                                                                                                MEDLINE=22341132; PubMed=12454917;
                                                   MEDLINE=22388257; PubMed=12477932;
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Pfam; PF00458; WHEP-TRS; 1.
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83.2%;
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Matches 333; Conservative
                                                                                                                                                                                                                     and mouse cDNA sequences.
        Xenopodinae, Xenopus.
NCBI_TaxID=8355;
Amphibia, Batrachia,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                  Richardson P.;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Last annotation update)
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PRINTS; PR01039; TRNASYNTHTRP.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
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Interpro; IPR001412; tRNA-synt_I.
Interpro; IPR002306; Trp_tRNA-synt_lb.
Pfam; PF00579; tRNA-synt_lb; 1.
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TISSUE-Profetate:

TRAUBETS R.D., Feingold E.A., Grouse L.H., Derge J.G.,

TRAUBETS R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Heilat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Aspleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McZwan P.J., McKernan K.J., Malek J.A., Gunaranche P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                    VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA 240
                                                                                                                                                                                                                             VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAVQAAPSFSNSFPKIFRDRTDIQCLIPCA 269
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                                                                                                                                      LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 180
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                   FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP
                                                                                                                                                        SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGGRPHH
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
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Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO61752; AAH61752.1; -.
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SEQUENCE 379 AA; 42880 MW; B9CDB2248780C2E1 CRC64;
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02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
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AAH61752;
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Length 379;

81.9%; Score 1734; DB 2; 92.2%; Pred. No. 1.2e-130;

Query Match Best Local Similarity

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STATEMENT OF TISSUE=Fye;

STRAIN=Wild-type'TISSUE=Fye;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

Ratasberg R.L., Felingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Antschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

An Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

An Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKerran K.J., Malek J.M., Gay L.J., Hulyk S.W.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Allalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,

R. Gones S.J., Marra M.A.,

R. Green E.D., Dickson M.C., Schein J.E.,

R. Gones S.J., Marra M.A.,

R. Green E.D., Schmutz J., Myers R.W., Schein J.E.,

R. Gones S.J., Marra M.A.,

R. Green E.D., Schmutz J., Myers R.W., Schein J.E.,

R. Gones S.J., Marra M.A.,

R. Gones S.J., Mar
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                        30 SNGDPDATKASEDFVDPWTVRTSSAKGIDYDKLIVQFGSSKIDKELINRIERATGQRPHR
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1 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
65-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein zgc:73274.
Name=zgc:73274;
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
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Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC059603; AAH59603.1; -.
InterPro; IPR009068; S15/NS1 bind.
InterPro; IPR002305; tRNA-synt_lb.
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STRAIN=Wild_type; TISSUE=Eye;
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MEDLINE-22388257; Pubmed=12477932;
Straubsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Straubsberg R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                       ATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGI
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
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                                                                                                                                                                                                                                                    Length 463;
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8; Pred. No. 1.5e-130;
42; Mismatches 30; Indels
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002306; Trp_tRNA-synt_lb.
InterPro; IPR000738; WHEP-TRS.
Pfam; PF00458; WHEP-TRS.
Pfam; PF00458; WHEP-TRS; I.
PRINTS; PR01039; TRNASYNTHTRP.
TIGREAMS; TIGR0233; trpS; I.
PROSITE; PS00178; ATRNA_LIGASE_I; I.
PROSITE; PS00178; ATRNA_LIGASE_I; I.
SRQUENCE 463 AA; 52372 MW; ED406A47C9628FEF CRC64;
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24-WAY-2004 (TrEMBLrel. 27, Last sequence update)
24-WAY-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein zgc:73274.
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320; Conservative
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Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marza M.A.; Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFGDRKDVQCLIPCAIDQDPY
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Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BC059603, HAP59603.1;
Hypothetical protein.
SEQUENCE 463 AA; 52372 MW; ED406A47C9628FEF CRC64;
                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 81.9%; Score 1734; DB 2; Best Local Similarity 81.6%; Pred. No. 1.5e-130; Matches 320; Conservative 42; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367 VLQPLIAEHQARRKEVTDEIVKEFMTPRKLSF 398
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Facent No. 6727066
GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
TITLE OF INVERTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: 60/222,113
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR PILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL PROGram
SEQ ID NO 163
LENGTH: 471
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Sequence 10919, A
Sequence 2, Appli
Sequence 2, Appli
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Sequence 2554, Ap
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Patent No. 6174713

GENERAL INFORMATION:
APPLICANT: Shen, Xiaoyu
APPLICANT: Houman, Fariba
TITLE OF INVENTION: SYNTHETASE PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING
TITLE OF INVENTION: SAME
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY. Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 ATAPTEDVVDPWNVASSNDAGVDYDKLIKRFGSSKIDEELIARFEXITGKPAHHFIRRGM 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 FFSHRDLHTILTLREQGKPFYLYTGRGPSSGSLHVGHLVPFIMTKWLQETFDVPLVIQLT 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 HVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQDPY 246
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                                                                                                          Sequence 45650, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 45650
LENGTH: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 ATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSGGRVTVEEHRKLGGVPEVDVSYQLLKFFLEDDAKLEEVRVAYSKGEMLTGEIKK 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 61.0%; Score 1290.5; DB 4; Length Best Local Similarity 67.4%; Pred. No. 3.6e-136; Matches 240; Conservative 51; Mismatches 64; Indels
                      KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 471
                                                                                                                                                                                                                                                                                                                                                                                                     ) OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45650
                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                       RESULT 2
US-09-270-767-45650
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US-08-876-885-26
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 61162
LENGTH: 210
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COMPUTER NEWSTERN FLORDY disk MEDIUM TYPE: Floppy disk MEDIUM TYPE: IBM PC compatible COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 SOFTWARE: Patentin Release #1.0, Version #1.30 SOFTWARE: US/08/876,885 FILING DATE: 16-JUN-1997 CLASSIFICATION NUMBER: US/08/876,885 ATTORNEY/AGENT INFORMATION: NAME: BLOCK, DAVIG E. REGISTRATION NUMBER: CP197-02 REFERENCE/DOCKET NUMBER: CP197-02 TELEPHONE: (781) 861-6240 TELEPHONE: (781) 861-6240 TELEPHONE: (781) 861-6240 TELEPHONE: (781) 861-6540 TELEPHONE: (781) 861-9540 TELEPHONE: (781) 861
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; Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Drosophila melanogaster
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Matches 226; Conservative
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US-08-876-885-26
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Sequence 7201, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: GTO99-03PA

CURRENT APPLICATION WUBBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               259 YPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKHAFSGGRDTIEEHR 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319 QFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELKKALIEVLQPLIAEHQAR 378
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                                        FOR DIAGNOSTICS AND THERAPEUTICS
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9.2%; Score 195; DB 4; L
Best Local Similarity 25.9%; Pred. No. 5.1e-13;
Matches 84; Conservative 56; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 550; DB 4;
Pred. No. 2.7e-53;
TITLE OF INVENTION: FOR DIAGNOSTICS AND THEMALE FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 19802
LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36; Mismatches
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RSKVDDQVVEKFMKPHKLVF 195
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53.0%;
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Best Local Similarity
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
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                                                                                                                                                                                                                                                                                                                                                  153 IACGFDINKTFIFSDLDYMGMSSGFYKNVVKIQKHVTFNQVKGIFGFTDSDCIGKISFPA
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                                                                                                                              Length 210;
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                                                                                                                                                                                                                    32; Indels
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                                                                                                                              DB 4;
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                                                                                                                         36.6%; Score 774.5; DB 4 68.6%; Pred. No. 1.4e-78; iive 33; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | |||||| ||||::| |: | |||||:||
LKFFLEDDAKLEEVRVAYSKGEMLTGEIKK 209
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                                                                                                                                                                  Best Local Similarity 68.69
Matches 144; Conservative
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Matches 125; Conservative
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US-09-248-796A-19803
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                                        US-09-270-767-61162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333
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                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273
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84 KPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKY-LWKDLTLDQAY 142
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                                                                                                                                                                                                              225 PADVLQKKV----MSMYTDPNHIHVQDPGQVEGNMVFTYLDVFGTDKEAIEEMKAHYRRG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 --FNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQC-LIPCAIDQDPY 246
                                      ----DITAFKANLVPVGEDOKPM 169
                                                                                                                      |::| |:|| | |:::|
170 LEQTQBIVQSFNHTYGEVLVEPKGVFPPKGMGR---LPGIDG-NGKWSKSLGN-GIYISD
                                                                                         -----VAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTD
                                                                                                                                                                                   294 TAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.8%; Score 185.5; DB 3;
Similarity 24.0%; Pred. No. 6.1e-12;
11; Conservative 60; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NATA:
CLASSIPICATION NATA:
CLASSIPICATION: 12-SEP-1997
CLASSIPICATION: 424
PRICR APPLICATION DATA:
APPLICATION NUMBER: 9619072.3
FILING DATE: 12-SEP-196
ATTOR APPLICATION NUMBER: 9619072.3
FILING DATE: 32-SEP-196
ATTOR APPLICATION NUMBER: 38,891
REGISTRATION NUMBER: 38,891
REFENCE/DOCKET NUMBER: P31624-1
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                        ::|:||:||:||:
281 GLGDVKIKRYLIDVLEAEFAPIRARREEL 309
                                                                                                                                                                                                                                                                               354 AMLTGELKKALIEVLOPLIAEHQARRKEV 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gentry, Danile
APPLICANT: Greenwood, Claire
APPLICANT: Greenwood, Claire
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: NO. 6046174el trpS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                              126 TEIEOKK----FGESVPTGFFIYPVSQAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/08928100
; Patent No. 6046174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 341 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 GDAVEN----
                                                                                            247 FRMTRD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: PA
COUNTRY: USA
ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Simi
Matches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-928-100-2
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                                                                                                                                                                                                                                                                                    Sequence 5765, Application US/09107532A
Patent No. 6583275
GENERAL INFORMITION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 NPEKVSSNVLQVALDYLAVGLDPAKSTLFIQSQIPELAELTWYYLNLVSVGRVRRNPTVK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 LYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKYLWKDLTLDQAYGDAVE 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N------KIQKHVI--FIFSDLDYMGMSSGFYKNVV---KIQKHVI-- 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 VNAMYTDPNHLRIEDPGGVEGN----IVPTYLDAFDPNKEEVEELKAHYRRGGLGDGTVK 279
                             VNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELK 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
8.8%; Score 186; DB 4; Length 348;
Best Local Similarity 24.9%; Pred. No. 5.5e-12;
Matches 82; Conservative 57; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ), NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...348
; SEQUENCE DESCRIPTION: SEQ ID NO: 5765:
US-09-107-532A-5765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5765:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Enterococcus faecium
                                                                                                                                                      280 KRLEGVLKELITPIRERREELAKD 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: <Unknown>
                                                                                                                           362 KALIEVLOPLIAEHOARRKEVTDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 348 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                   US-09-107-532A-5765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE
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213 LADDADTLRKKVMSMYTDPDHIRVEDPGKIEGN----WVFHYLDVFGRPEDAQEIADMKE 268
                                                                      245 PYFRMTRD------VAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIF 290
                                                                                                                                                                                                                                                          PMIEQTREIVRSFNNAYNCDVLVEPEGIYPENE--RAGRLPGLDG-NAKMSKS-LNNGIY 212
                                                                                                                                                                                                                                                                                                          291 LIDIAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFF--LEDDDKLEQIRK 348
                                           143 GDAVEN-----AKDIIACGFDINKTFIF--SDLDYMGMSSGFYKNVV---KIQK 186
                                                                                                                                 187 HVTFNQVKGIFGFTDSDCIGKISFPAIQAA--PSFSNSFPQIFRDRTDIQCLIPCAIDQD 244
  ----VLLQEEDKYDMFVFLADQQAL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                 349 DYTSGAMLTGELKKALIEVLQPLIAEHQARRKEVTDEI 386
                                                                                                                                                                                                                                                                                                                                                                                                                          269 RYQRGGLGDVKTKRYLLEILERELGPIRERRIEFAKDM 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
8.8%; Score 185.5; DB 4;
Best Local Similarity 24.0%; Pred. No. 6.1e-12;
Matches 81; Conservative 60; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09425666
Patent No. 6416976
GENERAL INFORMATION:
APPLICANT: Gentry, Danile
APPLICANT: Grenwood, Claire
APPLICANT: Grenwood, Claire
APPLICANT: Lawlor, Blizabeth
TITLE OF INVENTION: No. 6416976el trpS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/425,666
  3 KPIIL-TGDRPTGK-LHIGHYVGSLKNR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P31624-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/928,100
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNAY AGENT. INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P316
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 341 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , TOPOLOGY: linear
, MOLECULE TYPE: protein
US-09-425-666-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: P1
COUNTRY:
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                                                                      ---VAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIF 290
                                                                                                                                                                        157 PMIEQTREIVRSFNNAYNCDVLVEPEGIYPENE--RAGRLPGLDG-NAKMSKS-LNNGIY 212
                                                                                                                                                                                                                   LTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFF--LEDDDKLEQIRK 348
                                                                                                                                                                                                                                                 50 TDHAKDPQTIVESIGNVALDYLAVGLDPNKSTIFIQSQIPELAELSMYYMNLVSLARLER 109
                                         187 HVTFNQVKGIFGFTDSDCIGKISFPAIQAA--PSFSNSFPQIFRDRTDIQCLIPCAIDQD 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 KPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKY-LWKDLTLDQAY 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
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8.8%; Score 185.5; DB 3; Length 341;
Best Local Similarity 24.0%; Pred. No. 6.1e-12;
Matches 81; Conservative 60; Mismatches 128; Indels 69
                                                                                                                                                                                                                                                                                                                                   269 RYQRGGLGDVKTKRYLLEILERELGPIRERRIEFAKDM 306
                                                                                                                                                                                                                                                                                                        349 DYTSGAMLTGELKKALIEVLQPLIAEHQARRKEVTDEI 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gentry, Danile
APPLICANT: Greenwood, Claire
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 6346409el trpS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEGO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/492,581
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION NUMBER: US/08/928,100
FILING DATE: 12-SEP-1997
APPLICATION NUMBER: 9619072.3
FILING DATE: 12-SEP-196
ATTORNEY/AGENI INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: 931624-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 341 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                             245 PYFRMTRD---
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STRANDEDNESS: si
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APPLICANT: LYND Doucette-Stamm et al
APPLICANT: LYND Doucette-Stamm et al
APPLICANT: LYND Doucette-Stamm et al
APPLICANT: LYND Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERCOCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REPERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1990-08-13
PRIOR FILING DATE: 1997-08-15
NUMBER: OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN VETBION 3.1
SEQ ID NO 5784
LENGTH: 335
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Sequence 39, Application US/08743130A
Settle No. 5871987
GENERAL INFORMATION:
APPLICANT: Sassanfar, Mandana
APPLICANT: Shen, Xiaoyu
APPLICANT: Tao, Nianibu
APPLICANT: Tao, Jianshi
APPLICANT: Tao, Jianshi
APPLICANT: Tao, Jianshi
APPLICANT: Tao, Jianshi
APPLICANT: Tao, Jianshi
APPLICANT: Tao, Jianshi
APPLICANT: Tao, Jianshi
APPLICANT: Tao, Jianshi
APPLICANT: Tao, Jianshi
APPLICANT: Houman, Fariba
TITLE OF INVENTION: CANDIDA TYROSYL-tRNA SYNTHETASE
TITLE OF INVENTION: AND STRAINS COMPRISING SAME
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESSE: Annilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 NPTVKABIBOKK----FGEGVPTGFFIYPVSOAA-------DITAFOANLVPVGE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DODPYFRMTRD-------VAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSS 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : || |: : :|:|| : :|| |: : || |: : || |: : || |: : || |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: :|| |: : :|| |: : :|| |: : :|| |: :|| |: : :|| |: :|| |: :|| |: :|| |: :|| |: : :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |
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Best Local Similarity 23.5%; Pred. No. 1.2e-10;
Matches 81; Conservative 59; Mismatches 123; Indels
349 DYTSGAMLTGELKKALIEVLQPLIAEHQARRKEVTDEI 386
                                        269 RYQRGGLGDVKTKRYLLEILERELGPIRERRIEFAKDM
                                                                                                                                                                                                                                              // Sequence 5784, Application US/09134000C
// Patent No. 6617156
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US-09-134-000C-5784
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US-08-743-130A-39
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TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pretumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATHOLO-07A
CURRENT PILIOS DATE: 2000-05-26
RIOR APPLICATION NUMBER: US/09/583,110
RIOR APPLICATION NUMBER: US 60/107,433
RROR FILING DATE: 1998-06-30
RRIOR APPLICATION NUMBER: US 60/085,131
RRIOR FILING DATE: 1998-05-12
RRIOR FILING DATE: 1998-05-12
RRIOR FILING DATE: 1997-07-02
ROMBER OF SEQ ID NOS: 5322
SEQ ID NO 4392
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                                                                                                                                                                                             : | : | : | : | : | 110 NPTVKTEISQKGFGESIPTGFLVYPIAQAADITAFKANY-------VPVGTDQK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                       PYFRMTRD------VAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIF 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 KPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKY-LWKDLTLDQAY 142
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   84 KPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKY-LWKDLTLDQAY 142
                                                                                                                                                 143 GDAVEN------AKDIIACGFDINKTFIF--SDLDYMGMSSGFYKNVV---KIQK 186
                                                                                                                                                                                                                                                                                              187 HVTFNQVKGIFGFTDSDCIGKISFPAIQAA--PSFSNSFPQIFRDRTDIQCLIPCAIDQD 244
                                                69;
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24.0%; Pred. No. 1e-11;
tive 59; Mismatches 129; Indels 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 RYQRGGLGDVKTKRYLLEILERELGPIRERRIEFAKDM 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 4392, Application US/09583110; Patent No. 6699703; GENERAL INFORMATION:
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Best Local Similarity
Matches 81; Conserv
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US-09-583-110-4392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 NVPLVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGF 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 IKDVLEKENRPVKIYWGTAPTGKP-HCGYFVPMIKLAHFLKAGCEVTVLLADLHAFLDNM 85
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PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.8%; Score 164.5; DB 2; Length 409; 20.7%; Pred. No. 1.9e-09; ve 59; Mismatches 132; Indels 107;
                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,130A
FILING DATE: 01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 VLDAYENK-KPFYLYTGRGPSSEAMHVGHLIPFI---
                                                                                                                                                             FILING DATE: 01-NOV-1966
CLASSIFICATION: 435
ATOMNES/ACTORNATION: NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REPERENCE/DOCKET NUMBER: CP195-12
TELEPHONE: (617) 861-6240
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ. ID NO: 39: SEQUENCE CHARACTERISTICS:
                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08743130A Patent No. 5871987 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sassanfar, Mandana
Gallant, Paul L.
Shen, Xiaoyu
Tao, Nianjun
Tao, Jianshi
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APPLICANT: Gallant, Paul L.
APPLICANT: Shen, Xiaoyu
APPLICANT: Tao, Nianjun
APPLICANT: Tao, Jianshi
APPLICANT: Houman, Fariba
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 20.7%
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Massachusetts
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TOPOLOGY:
US-08-743-130A-39
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86 KAPLEVVKYRAKYYEFVVKAILKSINVPIERLKFVVGSSYQKGGDYV---MDLFKLSNIV 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 107;
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.7%; Score 162.5; DB 2; Best Local Similarity 20.7%; Pred. No. 3.2e-09; Matches 78; Conservative 59; Mismatches 132;
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Job time : 42 Becs
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CF195-12
TELECHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR ESQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/743,130A
FILING DATE: 01-NOV-1996
CLASSIFICATION: 435
                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA
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                                                                                                          Lexington
Massachusetts
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                                                                                                                                                                 USA
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                                                                                                                                     STATE: Ma
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Sequence 10, Appl.
Sequence 11, Appl.
Sequence 10, Appl.
Sequence 10, Appl.
Sequence 163, App.
Sequence 1235, App.
Sequence 1235, App.
Sequence 1236, App.
Sequence 12, Appl.
Sequence 16, Appl.
Sequence 120838,
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Sequence 12083,
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Sequence 12083,
Sequence 1208,
Sequence 1319,
Sequence 1319,
Sequence 1319,
Sequence 14889,
Sequence 1488,

4 US-10-080-839-1 5 US-10-240-532-10 6 US-10-240-532-10 6 US-10-240-631-165 6 US-10-240-671-166 6 US-10-733-963A-62 105-09-925-302-558 105-09-925-302-558 105-09-925-302-558 105-09-925-302-558 105-09-925-302-558 105-09-913-718-16 105-09-813-718-16 105-09-813-718-16 105-09-813-718-16 105-09-813-718-16 105-09-813-718-16 105-09-813-718-16 105-09-813-718-16 105-09-813-718-16 105-09-813-718-16 105-09-813-718-16 105-09-813-718-718-16 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-302-855 105-09-925-3

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Sequence 13. Application US/10080839

| Sequence 13. Application No. US20030017564A1
| Sebication No. US20030017564A1
| GENERAL INFORMATION: Schimmed, Paul
| APPLICANT: Schimmed, Paul
| APPLICANT: Wakasugi, Keisuke
| APPLICANT: Priedlander, Martin
| TITLE OF INVENTION: Polypeptides Useful For The Regulation of Angiogenesis
| TITLE OF INVENTION: Polypeptides Useful For The Regulation of Angiogenesis
| TITLE OF INVENTION: Polypeptides Useful For The Regulation of Angiogenesis
| TITLE OF ILLING DATE: 2002-02-22
| CURRENT FILING DATE: 2001-02-23
| NUMBER OF SEQ ID NOS: 13
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 13
| LENGTH: 401
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Best Local Similarity 100.0%; Pred. No. 3.9e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0;
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ORGANISM: Homo sapiens
US-10-080-839-13
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Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 21, Appl
Sequence 2134, Ap
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                                                                                                    January 10, 2005, 21:23:09; Search time 145 Seconds (without alignments) 997.166 Million cell updates/sec
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Sequence 5, Ap
Sequence 14, A
                                                                                                                                                                                                1 SNHGPDATEAEEDFVDPWTV......VTDEIVKEFWTPRKLSFDFQ 401
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18: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

19: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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10: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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2116
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Maximum Match 100%
Listing first 45 summaries
                                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Publication No. US20040009163A1
GENERAL INFORMATION:
APPLICANT: Schimmel, Paul
APPLICANT: Wakasugi, Keisuke
TITLE OF INVENTION: Human Aminoacyl-tRNA Syntherase Polypeptides Useful For
TITLE OF INVENTION: The Regulation of Anglogenesis
FILE REPERENCE: TSRI 1020/10240,532
CURRENT APPLICATION NUMBER: US/10/240,532
CURRENT FILING DATE: 2002-09-30
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Best Local Similarity 100.0%; Score 2116; DB 14; Length 415;
Best Local Similarity 100.0%; Pred. No. 4.1e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0;
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US-10-240-532-14
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US-10-080-839-5
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Publication No. US200201826681

GENERAL INFORMATION

APPLICANT: Schimmel, Paul

APPLICANT: Schimmel, Paul

TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For

TITLE OF INVENTION: The Regulation of Angiogenesis

FILE REPERENCE: 00-221

CURRENT APPLICATION NUMBER: US/09/813,718

CURRENT PILING DATE: 2001-03-21

SOFTWARE: Patentin Ver. 2.0
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100.0%; Pred. No. 4.1e-194;
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 401; Conservative
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LENGTH: 419
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Publication No. US20040152079A1
General InfoRMATION:
APPLICANT: SCHIMMEL, Paul
APPLICANT: SCHIMMEL, Paul
APPLICANT: WAKASUGI, Keisuke
ITILE OF INVENTION: Human Aminoacyl-tRNA Synthetase
ITILE OF INVENTION: Polypeptides Useful for the Regulation of Angiogenesis
FILE REFERENCE: TSRI 720.2
CURRENT APPLICATION NUMBER: US/10/240,527A
CURRENT APPLICATION NUMBER: PCT/US01/08966
PRIOR FILING DATE: 2000-09-30
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 415
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                                                                                                                                                                                                                                                                                                    415;
                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: human OTHER INFORMATION: supermini TrpRS in pET20B
                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                  100.0%; Score 2116; DB 15; 100.0%; Pred. No. 4.1e-194;
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US-10-240-527A-14
                                                                                                                                                                                                                                                                                                                                         0; Mismatches
PRIOR APPLICATION NUMBER: PCT/US01/08975
PRIOR APPLICATION NUMBER: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/193,471
PRIOR APPLICATION NUMBER: 2000-03-31
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
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ORGANISM: Artificial Sequence
                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 401; Conservative
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US-10-240-527A-14
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APPLICANT: Schimmel, Paul
APPLICANT: Schimmel, Reisuke
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
TITLE OF INVENTION: The Regulation of Angiogenesis
FILE REFERENCE: 00-221
CURRENT APPLICATION NUMBER: US/09/813,718
CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
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                                                                                                                    1 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGORPHH
                                                                                                                                                                         2 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH
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US-09-813-718-12
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Query Match
100.0%; Score 2116; DB 16;
Best Local Similarity 100.0%; Pred. No. 4.1e-194;
Matches 401; Conservative 0; Mismatches 0;
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Publication No. US20020182666A1
GENERAL INFORMATION:
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Matches 401; Conservative
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TYPE: PRT
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VVKIOKHVTFNOVKGIFGFTDSDCIGKISFPAIOAAPSFSNSFPOIFRDRTDIOCLIPCA

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Sequence 12, Application US/10240532
Sequence 12, Application US/10240532
Publication No. US20040009163A1
GENERAL INFORMATION:
APPLICANT: Schimmel, Paul
APPLICANT: Wakasugi, Keisuke
TITLE OF INVENTYON: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
TITLE OF INVENTYON: The Regulation of Anglogenesis
FILE REFERENCE: TSR 720.1
CURRENT APPLICATION NUMBER: US/10/240,532
CURRENT APPLICATION NUMBER: DCT/US01/08975
PRIOR APPLICATION NUMBER: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/193,471
PRIOR APPLICATION NUMBER: US 60/193,471
PRIOR APPLICATION NUMBER: 2000-03-31
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn Ver. 2.0
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Publication No. US20040152079A1
GENERAL INFORMATION:
APPLICANT: SCHIMMEL, Paul
APPLICANT: WAKASUGI, Keisuke
TITLE OF INVENTION: Polypeptides Useful for the Regulation of Angiogenesis
TITLE OF INVENTION: Polypeptides Useful for the Regulation of Angiogenesis
CURRENT APPLICATION NUMBER: US/10/240,527A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: human mini
OTHER INFORMATION: TYPRS in pET20B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 2116; DB 15; Length 437; 100.0%; Pred. No. 4.4e-194; ive 0; Mismatches 0; Indels 0;
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ORGANISM: Artificial Sequence
FEATURE:
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Matches 401; Conservative
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APPLICANT: Schimmel, Reisuke
APPLICANT: Wakasugi, Keisuke
APPLICANT: Wakasugi, Keisuke
APPLICANT: Wakasugi, Keisuke
APPLICANT: Priedlander, Martin
TITLE OF INVENTION: Tryptophanyl-trNA Synthetase Derived
TITLE OF INVENTION: Polypeptides Useful For The Regulation of Angiogenesis
FILE REPERENCE: TSRL-813.1
CURRENT APPLICATION WHBER: US/10/080,839
CURRENT FILING DATE: 2002-22
PRIOR APPLICATION NUMBER: 60/270,951
PRIOR APPLICATION NUMBER: 60/270,951
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFKDRTDIQCLIPCA 263
                                                                 241 IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
                                                                                          IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 323
                                                                                                                                                                                       KVNKHAFSGGRDTIEEHRQFGGRCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 383
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Best Local Similarity 100.0%; Pred. No. 4.4e-194;
Matches 401; Conservative 0; Mismatches 0;
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US-10-080-839-3
                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 3, Application US/10080839; Publication No. US20030017564A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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LENGTH: 437
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US-10-080-839-3
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Pred. No. 4.9e-194;
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APPLICANT: Afaz, Netesha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
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Hevezi, Peter A.
Mack, David H.
                 Matches 401; Conservative
 Best Local Similarity
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| Sequence 2, Application No. US20030059797A1
| GENERAL INFORMATION:
| APPLICANT PAILEY, Elena
| TITLE OF INVENTION: ANIMAL MODEL OF AND TEST FOR ALZHEIMER'S DISEASE
| FILE REFERENCE: PALL-11
| CURRENT FILING DATE: 2002-11-19
| CURRENT FILING DATE: 2001-04-19
| PRIOR APPLICATION NUMBER: 60/284,980
| PRIOR FILING DATE: 2001-04-19
| PRIOR FILING DATE: 2001-02-28
| PRIOR APPLICATION NUMBER: 09/513,895
| PRIOR FILING DATE: 1999-08-27
| NUMBER OF SEQ ID NOS: 6
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                            1 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH
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100.0%; Pred. No. 4.4e-194;
tive 0; Mismatches 0;
                                                                                                                                                                                                     , OTHER INFORMATION: Human mini TrpRS in pET20B
US-10-240-527A-12
          PRIOR APPLICATION NUMBER: PCT/US01/08966
PRIOR FILING DATE: 2001-03-21
PRIOR PILICATION NUMBER: US 60/193,471
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PRELSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 437
 2002-09-30
                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-126-467B-2
CURRENT FILING DATE:
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hes 401; Conserv
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Best Local S:
Matches 401
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100.0%; Score 2116; DB 14; Length 471;

Query Match

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APPLICANT: Mateon, Suean R.
APPLICANT: Wateon, Suean R.
APPLICANT: Wateon, Suean R.
APPLICANT: Wateon, Suean R.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Screening for Modulators of Cancer CURRENT FILING DATE: 2002-11-13
FRIOR PRIOR PELICATION NUMBER: US 60/35,027
CURRENT APPLICATION NUMBER: US 60/35,666
FRIOR PRIOR APPLICATION NUMBER: US 60/35,666
FRIOR FILING DATE: 2001-11-13
FRIOR FILING DATE: 2001-11-12
FRIOR FILING DATE: 2001-11-12
FRIOR FILING DATE: 2001-11-29
FRIOR FILING DATE: 2001-11-29
FRIOR FILING DATE: 2001-11-24
FRIOR FILING DATE: 2001-11-24
FRIOR FILING DATE: 2001-11-24
FRIOR FILING DATE: 2001-11-24
FRIOR FILING DATE: 2002-01-08
FRIOR FILING DATE: 2002-01-08
FRIOR FILING DATE: 2002-01-08
FRIOR FILING DATE: 2002-01-08
FRIOR FILING DATE: 2002-02-03
FRIOR FILING DATE: 2002-02-03
FRIOR FILING DATE: 2002-02-03
FRIOR APPLICATION NUMBER: US 60/347,319
FRIOR FILING DATE: 2002-02-03
FRIOR APPLICATION NUMBER: US 60/355,714
FRIOR FILING DATE: 2002-02-03
FRIOR APPLICATION NUMBER: US 60/356,714
FRIOR FILING DATE: 2002-02-03
FRIOR APPLICATION NUMBER: US 60/356,714
FRIOR FILING DATE: 2002-02-03
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   Gaps
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Remaining Prior Application data removed - See File Wrapper or PALM.
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0; Mismatches
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11 SNHGPDATEAEEDFVDFWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH 130
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131 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP 190
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                                                           LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN
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APPLICANT: BODARY, SARAH C.
APPLICANT: CLARK, HILLARY

APPLICANT: BRISDELL, HUNTE

APPLICANT: SCHOENFELD, JILL R.
APPLICANT: SCHOENFELD, JILL R.
APPLICANT: WOLD, WILLIAMS, P. MICKEY

APPLICANT: WOLD, WILLIAMS, P. MICKEY

APPLICANT: WOLVENTION: Compositions and Methods for the Treatment of I

TITLE OF INVENTION: Compositions and Methods for the Treatment of I

TITLE OF INVENTION: Related Diseases

FILE REFERENCE: P1948R1-US

CURRENT APPLICATION NUMBER: US/10/370,715B

CURRENT FILING DATE: 2003-02-21

NUMBER OF SEQ ID NOS: 742

SEQ ID NO SEO
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// Publication No. US20040258678A1
// GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 401; Conservative
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US-10-370-715B-250
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TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
TITLE OF INVENTION: PATHWAY
FILE REPERENCE: D0284 NP
CURRENT APPLICATION NUMBER: US/10/755,889
CURRENT PILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: U.S. 60/440,068
PRIOR PELING DATE: 2003-01-14
PRIOR PLING DATE: 2003-01-12
NUMBER OF SEQ ID NOS: 823
SOFTWARE: Patentin Version 3.2
SEQ ID NOS: 823
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llarity 100.0%; Pred. No. 4.9e-194;
Conservative 0; Mismatches 0; 1
                                                                                                                                                            100.0%; Score 2116; DB 14; 100.0%; Pred. No. 4.9e-194;
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                      SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1234
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      NUMBER OF SEQ ID NOS: 1386
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ORGANISM: Homo sapiens
                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1234
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US-10-755-889-250
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APPLICANT: Wakasudi, Ketsuke
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
TITLE OF INVENTION: The Regulation of Angiogenesis
FILE REPERBNCE: 00-221
CURRENT APPLICATION NUMBER: US/09/813,718
CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
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                                                                                431 KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 471
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; Sequence 10, Application US/09813718
; Publication No. US20020182666A1
; GENERAL INFORMATION:
; APPLICANT: Schimmel, Paul
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ORGANISM: Artificial Sequence
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Useful For The Regulation of Angiogenesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 2116; DB 14; Length 484; Best Local Similarity 100.0%; Pred. No. 5.1e-194; Matches 401; Conservative 0; Mismatches 0; Indels 0;
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TITLE OF INVENTION: Tryptophanyl-tRNA Synther
TITLE OF INVENTION: Polypeptides Useful For
FILE REFERENCE: TSRI -813.1
CURRENT APPLICATION NUMBER: US/10/080,839
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 60/270,951
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Recombinant human trpRS US-10-080-839-1
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